

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:41:31 ; Search time 159 Seconds
(without alignments)

1263.449 Million cell updates/sec

Title: US-09-853-880A-17

Perfect score: 3026

Sequence: 1 MECLYYFLGFLLLAARLPD.....FPGNQEKDPLLNQEPKGV 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep_23Sep04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3026	100.0	560	2 AAW35382	Murine me
2	3026	100.0	560	3 AAB11329	PA
3	3026	100.0	560	5 ABB78200	Abb78200 Amino aci
4	3026	100.0	560	5 ABB74961	Abb74961 Human lun
5	3026	100.0	560	5 ABP61881	Abp61881 Human lun
6	3026	100.0	560	6 ABUS6592	Abu56592 Lung canc
7	3026	100.0	560	6 ABG72362	Abg72362 Human set
8	3026	100.0	560	6 ABU70852	Abu70852 Human adi
9	3026	100.0	560	7 ADA28315	Ada28315 Human lun
10	3026	100.0	560	7 ADE95620	Ad95620 Human NOV
11	3026	100.0	560	7 ADH36879	Adh36879 Human lun
12	3026	100.0	560	7 ADJ68660	Adj68660 Human bea
13	3026	100.0	560	7 ADL14995	Adl14995 Human NMB
14	3026	100.0	560	7 ADN39940	Adn39940 Cancer/an
15	3026	100.0	560	8 ADH56342	Adh56342 Human nmb
16	3026	100.0	560	8 ADJ75569	Adj75569 Marker ge
17	3026	100.0	560	8 ADM56682	Adm56682 Human lun
18	3026	100.0	560	8 ADQ18310	Adq18310 Human sof
19	3007	99.4	572	7 ADU78235	Adu78235 Human CGD
20	3006	99.3	572	5 AAU83612	Aau83612 Human PRO
21	3006	99.3	572	6 ABU80759	Abu80759 Human PRO
22	3006	99.3	572	6 ABO33725	Ab33725 Novel hum
23	3006	99.3	572	6 ABU82068	Abu82068 Novel hum
24	3006	99.3	572	6 ABJ72248	Abj72248 Human PRO
25	3006	99.3	572	6 ABJ72376	Abj72376 Human PRO

ALIGNMENTS

RESULT 1

AAW35382
ID AAW35382 standard; protein; 560 AA.

XX AC AAW35382;

XX DT 26-FEB-1998 (first entry)

XX DE Murine metastatic nucleic acid sequence product.

XX KW Mouse; murine; tumour; cancer; metastatic sequence; detection; diagnosis; treatment; metastasis; hyperplasia; dysplasia; hypertrophy; screening.

XX OS Mus musculus.

XX PN WO9718454-A2.

XX PD 22-MAY-1997.

XX PF 15-NOV-1996; 96WO-US018567.

XX PR 16-NOV-1995; 95US-0006838P.

XX PR 30-JAN-1996; 96US-00594031.

XX (THOM/) THOMPSON T.

XX Thompson T;

XX WPI; 1997-289397/26.

PT Identifying tumour metastatic sequences - by introducing transfected cells into host mammal and analysing primary and metastatic sequences by differential display PCR.

PS Disclosure; Fig 12CI; 102pp; English.

XX Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mouse embryos. The UGS cells were infected with retroviruses, cultured and implanted under the renal capsule of mice. Reconstitutions were harvested 5 weeks later, when they showed signs of distress from the tumour burden. Metastatised tumours were isolated from a site outside the renal capsule. RNA was isolated from primary tumours and metastases, reverse transcribed and subjected to differential display PCR. The sequences were analysed to obtain metastatic sequences, e.g. the sequence encoding the present CC related to metastasis, or treat malignant or non-malignant disorders, CC e.g. hyperplasia, dysplasia and hypertrophy. The metastatic sequence can be used to screen a biological sample for metastasis, and it or its

CC expression product may also be used to treat a metastatic disorder

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFGLGFLLLAARLPLDAAKRFHDLGNRPSAYMREHNQNGSSDENDWNEKLYP 60
Db 1 MECLYFGLGFLLLAARLPLDAAKRFHDLGNRPSAYMREHNQNGSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSKGRGVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSKGRGVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDQKPPPHPGWRWNFIYVFTL 180
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDQKPPPHPGWRWNFIYVFTL 180
QY 181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVFV 240
Db 181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVFV 240
QY 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
QY 361 RYGHFQATITIVEGILEVNIIOQMTDVLMPVPWPESSLIDFVVTCCGSIPTVCTIISDPT 420
Db 361 RYGHFQATITIVEGILEVNIIOQMTDVLMPVPWPESSLIDFVVTCCGSIPTVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLKNQEFKGV 560
Db 541 FPGNQEKDPLLKNQEFKGV 560

RESULT 2

AAB11329
ID AAB11329 standard; protein; 560 AA.

XX AC AAB11329;

XX DT 21-FEB-2001 (first entry)

XX DE Human lung cancer-associated protein L528S.

XX KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX KW vaccine; detection.

XX OS Homo sapiens.

XX FN WO200061612-A2.

XX PD 19-OCT-2000.

XX PF 03-APR-2000; 2000WO-US008896.

XX PR 02-APR-1999; 99US-00285479.

XX PR 17-DEC-1999; 99US-00466396.

XX PR 30-DEC-1999; 99US-00476496.

PR 10-JAN-2000; 2000US-00480884.
PR 22-FEB-2000; 2000US-00510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient.

XX Claim 3; Page 203-204; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 3; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYFGLGFLLLAARLPLDAAKRFHDLGNRPSAYMREHNQNGSSDENDWNEKLYP 60
Db 1 MECLYFGLGFLLLAARLPLDAAKRFHDLGNRPSAYMREHNQNGSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSKGRGVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSKGRGVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDQKPPPHPGWRWNFIYVFTL 180
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDQKPPPHPGWRWNFIYVFTL 180
QY 181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVFV 240
Db 181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVFV 240
QY 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
QY 361 RYGHFQATITIVEGILEVNIIOQMTDVLMPVPWPESSLIDFVVTCCGSIPTVCTIISDPT 420
Db 361 RYGHFQATITIVEGILEVNIIOQMTDVLMPVPWPESSLIDFVVTCCGSIPTVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLKNQEFKGV 560
Db 541 FPGNQEKDPLLKNQEFKGV 560

	Query Match	100.0%;	Score 3026;	DB 5;	Length 560;	
	Best Local Similarity	100.0%;	Pred. No. 4.7e-262;			
	Matches 560;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1	MECLYYFLGFLLLAARLPDAAKRFHDLVGNRP	SAYNREHNQLNWSSDENDNNEKLYP	60		
Db	1	MECLYYFLGFLLLAARLPDAAKRFHDLVGNRP	SAYNREHNQLNWSSDENDNNEKLYP	60		
Qy	61	VWKGDMRWKNSKGGKGRVQAVLTSDSPALVGSNITFAVNLIFPPRCQKEDANGNIIVYEKNC	120			
Db	61	VWKGDMRWKNSKGGKGRVQAVLTSDSPALVGSNITFAVNLIFPPRCQKEDANGNIIVYEKNC	120			

PS Disclosure; Page 281-283; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies, fusion

CC proteins, T cell populations, or antigen presenting cells that express

CC the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

CC invention

XX

SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 5; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60

Db 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60

QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120

Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120

QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNFIYVFTL 180

Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNFIYVFTL 180

QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVVTDDQIPVFV 240

Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVVTDDQIPVFV 240

QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPSEHFNSTINYKWSFGDNTGLFVSTNHTVN 300

Db 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPSEHFNSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVINGTFSNLNITVKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360

Db 301 HTYVINGTFSNLNITVKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360

QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420

Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420

QY 421 CEITONTVCSPVDVDENCCLLTVRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPAS 480

Db 421 CEITONTVCSPVDVDENCCLLTVRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPAS 480

QY 481 PLRMANSALISVGCIAIFVTVISLLVYKKGKEYNPINSPGNVVRSGLSVFLNRAKAVF 540

Db 481 PLRMANSALISVGCIAIFVTVISLLVYKKGKEYNPINSPGNVVRSGLSVFLNRAKAVF 540

QY 541 FPGNQEKPDLKKNQEPKGV 560

Db 541 FPGNQEKPDLKKNQEPKGV 560

RESULT 5

ABP61881

ID ABP61881 standard; protein; 560 AA.

XX

AC ABP61881;

XX

DT 07-OCT-2002 (first entry)

DE Human lung cancer associated protein sequence SEQ ID NO:225.

XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX

PN WO200247534-A2.

XX 20-JUN-2002.

PD 30-NOV-2001; 2001WO-US047576.

PF 12-DEC-2000; 2000US-00735705.

PR 07-MAY-2001; 2001US-00850716.

PR 28-JUN-2001; 2001US-00897778.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Retter MW, Durham M, Fanger GR, Vedvick TS;

PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

XX WPI; 2002-583465/62.

XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded by

PT the polynucleotides, useful in pharmaceutical compositions such as

PT vaccines and as markers to indicate the presence of lung cancer.

XX

XX Example 1; Page 289-290; 381pp; English.

PS The present invention describes isolated human lung carcinoma

CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic

CC activity, and can be used in gene therapy and in vaccines. Compositions

CC comprising (I) or (II) can be used for stimulating an immune response in

CC a patient and for treating lung cancer in a patient. Oligonucleotides of

CC (I) can be used for detecting the presence of a cancer in a patient, by

CC obtaining a biological sample from the patient, contacting the biological

CC sample with the oligonucleotide, detecting in the sample, an amount of

CC polynucleotide that hybridises to the oligonucleotide and comparing the

CC amount of polynucleotide that hybridises to the oligonucleotide to a

CC predetermined cut-off value, and determining the presence of a cancer in

CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.

CC vaccines. (I) is useful as a marker to indicate the presence or absence

CC of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to

CC ABP61992 represent sequences used in the exemplification of the present

CC invention

XX

SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 5; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60

Db 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60

QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120

Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120

QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNFIYVFTL 180

Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNFIYVFTL 180

QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVVTDDQIPVFV 240

Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVVTDDQIPVFV 240

QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPSEHFNSTINYKWSFGDNTGLFVSTNHTVN 300

Db 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPSEHFNSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVINGTFSNLNITVKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360

Db 301 HTYVINGTFSNLNITVKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360

QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420

Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420

Db 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGISPTVETCTIISDPT 420
Qy 421 CEITQNTVCS PVDVDEMCLLTVRTFNGSGTYCVNLTGDDTSLALTSTLISVPRDRPAS 480
Db 421 CEITQNTVCS PVDVDEMCLLTVRTFNGSGTYCVNLTGDDTSLALTSTLISVPRDRPAS 480
Qy 481 PLRMANSALISVGCLAI FVTVISLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCLAI FVTVISLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Qy 541 FPGNQEKDPLLNQEFKGV 560
Db 541 FPGNQEKDPLLNQEFKGV 560

RESULT 6

ID ABUS6592 standard; protein; 560 AA.
XX AC

XX AC ABUS6592;

XX DT 02-APR-2003 (first entry)

XX XX Lung cancer-associated polypeptide #185.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX XX WO200286443-A2.

XX XX 31-OCT-2002.

XX XX 18-APR-2002; 2002WO-US012476.

XX XX 18-APR-2001; 2001US-0284770P.

XX XX 09-NOV-2001; 2001US-0290492P.

XX XX 13-NOV-2001; 2001US-0339245P.

XX XX 29-NOV-2001; 2001US-0350666P.

XX XX 12-APR-2002; 2002US-0372246P.

XX XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR N-PSDB; ABX76321.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient

XX PT for treating lung cancer, by contacting a biological sample from the

XX PT patient with a polynucleotide that exhibits increased or decreased

XX PT expression in lung cancer.

XX PS Claim 27; Page 328; 453pp; English.

XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention

XX SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 6; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECLYFFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60

Db 1 MECLYFFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60

Qy 61 VKRGDMWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYKNC 120

Db 61 VKRGDMWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYKNC 120

Qy 121 RNEAGLSADPYVYNWWTAMSEDSGNGTGQSHHNVFPDGKPPHHPGRRRNFIYVFTL 180

Db 121 RNEAGLSADPYVYNWWTAMSEDSGNGTGQSHHNVFPDGKPPHHPGRRRNFIYVFTL 180

Qy 181 GQYFQKLGRCVRSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTDOIPVFV 240

Db 181 GQYFQKLGRCVRSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTDOIPVFV 240

Qy 241 TMFQKNDNRNSDENTFLKDLPTMEDVLIHDPSEFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300

Db 241 TMFQKNDNRNSDENTFLKDLPTMEDVLIHDPSEFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300

Qy 301 HTYVLNGTFSNLNLTAKAAAGCPPPPPPPPSKPTPSLGPAGDNPLSLRIPDENCIN 360

Db 301 HTYVLNGTFSNLNLTAKAAAGCPPPPPPPPSKPTPSLGPAGDNPLSLRIPDENCIN 360

Qy 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGISPTVETCTIISDPT 420

Db 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGISPTVETCTIISDPT 420

Qy 421 CEITQNTVCS PVDVDEMCLLTVRTFNGSGTYCVNLTGDDTSLALTSTLISVPRDRPAS 480

Db 421 CEITQNTVCS PVDVDEMCLLTVRTFNGSGTYCVNLTGDDTSLALTSTLISVPRDRPAS 480

Qy 481 PLRMANSALISVGCLAI FVTVISLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

Db 481 PLRMANSALISVGCLAI FVTVISLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

Qy 541 FPGNQEKDPLLNQEFKGV 560

Db 541 FPGNQEKDPLLNQEFKGV 560

RESULT 7

ABG72962

ID ABG72962 standard; protein; 560 AA.

XX AC ABG72962;

XX DT 08-APR-2003 (first entry)

XX XX Human osteoactivin homologue, nmb.

XX KW Human; osteoactivin; osteopathic; antiinflammatory; vaccine;

XX KW bone cell differentiation stimulator; gene therapy; bone formation;

XX KW osteoporosis; periodontal disease; ectopic bone formation; osteopetrosis;

XX KW bone disorder; osteogenesis; enzyme.

XX OS Homo sapiens.

XX XX US2002151486-A1.

XX XX

PD 17-OCT-2002.
XX
PF 30-AUG-2001; 2001US-00943075.
XX
PR 30-AUG-2000; 2000US-0229006P.
XX
PA (POPO/) POPOFF S N.
PA (SAFA/) SAFADI F F.
PA (OWEN/) OWEN T A.
PA (SMOC/) SMOCK S L.
XX
PI Popoff SN, Safadi FF, Owen TA, Smock SL;
XX WPI; 2003-182528/18.
DR
PT Novel isolated osteoactivin protein and gene encoding the protein, useful
PT for stimulating bone differentiation and for treating bone disorders
PT including osteoporosis and periodontal disease.
XX
PS Claim 24; Fig 2B; 38pp; English.
XX
CC The invention describes an isolated and substantially pure osteoactivin
CC protein (I) that stimulates bone cell differentiation. A therapeutic
CC composition comprising (I), the polynucleotide (I) encoding (I) or a
CC biologically active fragment of (I) is useful for stimulating bone
CC formation in a mammal. The composition of (I) is useful for treating a bone
CC disorder including osteoporosis and periodontal disease. A second
CC therapeutic composition comprising an anti-(I)-antibody or an agent that
CC inhibits osteoactivin-mediated bone formation is also useful for inhibiting
CC formation in a mammal. The second composition is also useful for treating
CC ectopic bone formation and osteopetrosis. (I) and (II) are also useful
CC for developing novel therapeutic compositions for bone disorders, and for
CC stimulating osteogenesis. The polynucleotide is also useful in gene
CC therapy. This is the amino acid sequence of human mmb, a homologue of the
CC rat osteoactivin of the invention used in the creation of antibodies for
CC detection of mmb and osteoactivin
XX
SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSPAYMRHNLGWSDDNDWNEKLYP 60
DB 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSPAYMRHNLGWSDDNDWNEKLYP 60
QY 61 VKRGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
DB 61 VKRGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNPIYVPHTL 180
DB 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDPGKPPHHPGWRWNPIYVPHTL 180
QY 181 GOYFQKLGCSVRVSVNTAVNTLGPOLMEVTVYRHGRAVPTAOKVDVYVTDQIPVFV 240
DB 181 GOYFQKLGCSVRVSVNTAVNTLGPOLMEVTVYRHGRAVPTAOKVDVYVTDQIPVFV 240
QY 241 TMEQKNDRNSDTEFLKDLPIFMDVLIHDSHFLNTSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMEQKNDRNSDTEFLKDLPIFMDVLIHDSHFLNTSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTVVLNGTSLNLTVAARPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIDENCQIN 360
DB 301 HTVVLNGTSLNLTVAARPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIDENCQIN 360
QY 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIVVTCQGSIPTEVCTIISDPT 420
DB 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIVVTCQGSIPTEVCTIISDPT 420
QY 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCNVLTGLDDTSLALTSLISVPDRDPAS 480
DB 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCNVLTGLDDTSLALTSLISVPDRDPAS 480
QY 481 PLRMANSALISVGCCLAIFVTVISLVYKHKHKEYNIENSPGNVRSKGLSVFLNRAKAYF 540
DB 481 PLRMANSALISVGCCLAIFVTVISLVYKHKHKEYNIENSPGNVRSKGLSVFLNRAKAYF 540
QY 541 PFGNOEKOPLLKNQBFKGSV 560
DB 541 PFGNOEKOPLLKNQBFKGSV 560

RESULT 8
ABU70852
ID ABU70852 standard; protein; 560 AA.
XX
AC ABU70852;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human adipocyte Selected Interacting domain, SID, #483.
XX
KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
KW antidiabetic; protein-protein interaction; diabetes;
KW yeast 2-hybrid assay; metabolic disorder; obesity.
XX
OS Homo sapiens.
XX
PN WO200286122-A2.
XX
PD 31-OCT-2002.
XX
PF 14-MAR-2002; 2002WO-BP003768.
XX
PR 14-MAR-2001; 2001US-0275734P.
XX
PA (HYBR-) HYBRIGENICS.
XX
PI Legrain P, Daviet L;
XX
DR WPI; 2003-103412/09.
DR N-PSDB; ACA57396.
XX
PT New complex between two interacting proteins in adipocyte cells, useful
PT for identifying selected interacting domains that modulate protein
PT interactions, or for preventing or treating metabolic disorders such as
PT obesity or diabetes.
XX
PS Claim 6; Page 269-270; 382pp; English.
XX
CC The invention relates to a complex between two interacting proteins in
CC adipocyte cells, given in the specification. The proteins are identified
CC by selecting a bait protein from a known adipocyte marker and then
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
CC members of an adipocyte cDNA library. The proteins are designated SID
CC (RTM) (selected interacting domains) proteins. Also included are a
CC polynucleotide encoding a polypeptide in the adipocyte cells, a
CC recombinant host cell expressing at least one of the interacting
CC polypeptides of the complex, selecting a modulating compound in adipocyte
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
CC sequences given in the specification (including its fragment or variant),
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
CC given in the specification (including its fragment or variant), a vector
CC comprising the SID (RTM) polynucleotide, a recombinant host cell
CC comprising the vector, a protein chip comprising the polypeptides and a
CC record comprising all or part of the data, listed in the specification.
CC The complex, polypeptides, polynucleotides and compounds are useful for
CC preventing or treating metabolic disorders such as obesity or diabetes.
CC The polynucleotides are useful as probes or primers. The complex is
CC particularly useful for identifying selected interacting domains (SID
CC (RTM)) for screening drugs that modulate the protein interaction, thus
CC exhibiting the therapeutic effect. The present sequence represents a SID
CC (prey) protein of the invention
XX

Db 361 RYGHFQATITVEGLEVINIQTDLMPVPPESSLIIDFVVTCQGSIPTEVCTIISDPT 420
Qy 421 CEITQNTVCSPVDVDEMCLLTVRRRTFNGSGTYCVNLTLDGDTSLALTSTLISVPRDRPAS 480
Db 421 CEITQNTVCSPVDVDEMCLLTVRRRTFNGSGTYCVNLTLDGDTSLALTSTLISVPRDRPAS 480
Qy 481 PLRMANSLISVGLCLAFVTVISLLVYKHKKEYNPIENSPGNVVRSGKLSVFLNRAKAVF 540
Db 481 PLRMANSLISVGLCLAFVTVISLLVYKHKKEYNPIENSPGNVVRSGKLSVFLNRAKAVF 540
Qy 541 PFGNQEKDPLLNQEFKGV 560
Db 541 PFGNQEKDPLLNQEFKGV 560
RESULT 10
ADE95620
ID ADE95620 standard; protein; 560 AA.
XX AC ADE95620;
XX DT 12-FEB-2004 (first entry)
XX DE Human NOVX28c protein.
XX KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX28c.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT FT Misc-difference 47
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Arg as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 57
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Glu as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 111
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Asp as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 130
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Pro as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 154
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Ser as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 162
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Leu as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 294
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Phe as a result of a
FT FT single nucleotide polymorphism"
FT FT Misc-difference 324
FT FT /label= OTHER
FT FT /note= "OTHER= May be substituted by Leu as a result of a
FT FT single nucleotide polymorphism"

FT Misc-difference 460
FT /label= OTHER
FT /note= "OTHER= May be substituted by Asp as a result of a
FT single nucleotide polymorphism"
FT Misc-difference 487
FT /label= OTHER
FT /note= "OTHER= May be substituted by Ser as a result of a
FT single nucleotide polymorphism"
FT Misc-difference 526
FT /label= OTHER
FT /note= "OTHER= May be substituted by Arg as a result of a
FT single nucleotide polymorphism"
XX WO2003050245-A2.
XX 19-JUN-2003.
XX 03-DEC-2002; 2002WO-US038594.
XX 05-DEC-2001; 2001US-0336600P.
XX 07-DEC-2001; 2001US-0338285P.
XX 12-DEC-2001; 2001US-0341346P.
XX 17-DEC-2001; 2001US-0341477P.
XX 17-DEC-2001; 2001US-0341540P.
XX 20-DEC-2001; 2001US-0342592P.
XX 27-DEC-2001; 2001US-0344297P.
XX 31-DEC-2001; 2001US-0344903P.
XX 17-APR-2002; 2002US-0373286P.
XX 15-MAY-2002; 2002US-0380981P.
XX 17-MAY-2002; 2002US-0381495P.
XX 28-MAY-2002; 2002US-0383534P.
XX 28-MAY-2002; 2002US-0383744P.
XX 29-MAY-2002; 2002US-0383829P.
XX 29-MAY-2002; 2002US-0384024P.
XX 07-AUG-2002; 2002US-0401788P.
XX 26-OCT-2002; 2002US-0406353P.
XX 31-OCT-2002; 2002US-00401788.
XX 02-DEC-2002; 2002US-00406353.
XX (CURA-) CURAGEN CORP.
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphey R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Stirling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
XX N-PSDB; ADE95619.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX Claim 2; SEQ ID NO 152; 211pp; English.
XX This invention relates to novel NOVX proteins, and the DNA sequence which
XX encode them, having properties related to stimulation of biochemical or
XX physiological responses in a cell, a tissue, an organ or an organism.
XX Compounds which modulate the proteins of the invention may have cardiant,
XX antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
XX antiarthritic, antidiabetic, nephrotropic, dermatological,
XX immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
XX nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
XX antidepressant, antiallergic or gynaecological activities. The DNA
XX sequences of the invention may be useful for gene therapy whilst the
XX protein sequences may allow the development of a vaccine. The protein is
XX useful in the manufacture of a medicament for treating a syndrome
XX associated with a human disease. The invention may be useful in
XX diagnosing, treating or preventing NOVX-associated disorders, for example
XX cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
XX rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin

CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the amino acid
 CC sequence of the human NOVX28c protein of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60
 Db 1 MECLYYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60
 QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
 Db 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
 QY 121 RNEAGLSADPYVYNTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180
 Db 121 RNEAGLSADPYVYNTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180
 QY 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYYVTTDQIPVFV 240
 Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYYVTTDQIPVFV 240
 QY 241 TMFQKNDNRNSDDETFKDLPIFMDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
 Db 241 TMFQKNDNRNSDDETFKDLPIFMDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
 QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
 Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
 QY 361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSGIPTVECTIISDPT 420
 Db 361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSGIPTVECTIISDPT 420
 QY 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTSLISVPRDRPAS 480
 Db 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTSLISVPRDRPAS 480
 QY 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
 Db 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
 QY 541 FPGNQEKDPLLNQOEFGKVS 560
 Db 541 FPGNQEKDPLLNQOEFGKVS 560

RESULT 11

ADH36879

ID ADH36879 standard; protein; 560 AA.

XX AC ADH36879;

XX AC ADH36879;

DT 11-MAR-2004 (first entry)

XX Human lung cancer-related protein #16.

DE lung cancer; lung tumour; immune response stimulation;

KW tumour protein specific T cell; human.

XX Homo sapiens.

OS WO2003086175-A2.

XX PD 23-OCT-2003.

XX

PF 07-APR-2003; 2003WO-US010945.

XX 05-APR-2002; 2002US-00117982.

PR 04-DEC-2002; 2002US-00313986.

XX (CORI-) CORIXA CORP.

XX Mericle B, Fanger GR, Vedvick TS, Carter D, Watanabe Y;

PI Henderson RA, Kalos MD, Spies GA, Foy TM, Fan L, McNabb A;

PI Reed SG;

XX WPI; 2003-845247/78.

DR

XX Use of compositions comprising lung tumor polypeptides or

PT polynucleotides, for inhibiting lung cancer or tumor progression,

PT stimulating immune response, or stimulating and/or expanding T cells

PT specific for a tumor protein.

XX Disclosure; SEQ ID NO 225; 456pp; English.

PS

XX The invention comprises a method for inhibiting the development of lung

CC cancer, the method involves the use of compositions which contain lung

CC tumour polypeptides/polynucleotides. The methods and compositions of the

CC invention are useful for inhibiting lung cancer development or tumour

CC progression, stimulating immune response, or stimulating and/or expanding

CC T cells specific for a tumour protein. The present amino acid sequence

CC represents a human lung cancer-related protein.

XX Sequence 560 AA;

QY

Query Match 100.0%; Score 3026; DB 7; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60

Db 1 MECLYYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60

QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120

Db 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120

QY 121 RNEAGLSADPYVYNTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180

Db 121 RNEAGLSADPYVYNTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180

QY 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYYVTTDQIPVFV 240

Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYYVTTDQIPVFV 240

QY 241 TMFQKNDNRNSDDETFKDLPIFMDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300

Db 241 TMFQKNDNRNSDDETFKDLPIFMDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360

Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360

QY 361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSGIPTVECTIISDPT 420

Db 361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSGIPTVECTIISDPT 420

QY 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTSLISVPRDRPAS 480

Db 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTSLISVPRDRPAS 480

QY 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

Db 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

QY 541 FPGNQEKDPLLNQOEFGKVS 560

Db 541 FPGNQEKDPLLNQOEFGKVS 560

PS Disclosure; SEQ ID NO 7; 342pp; English.

XX The invention relates to a compound comprising a binding moiety which selectively binds to a protein or polypeptide listed in the specification (e.g. human autotaxin polypeptide or human CD24 signal transducer polypeptide), and a further moiety. The compound is useful in medicine or in the treatment, imaging, diagnosis or prognosis of mantle cell lymphomas (MCL). It is used in preparing a medicament for treating MCL, a diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells in the body of an individual. This sequence corresponds to one of the polypeptides of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60

QY 61 VMKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120
DB 61 VMKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120

QY 121 RNEAGLSADPYNNWTAWSESDGNGTGQSHHNVFPDCKPFPHPGWRWNIYVFHTL 180
DB 121 RNEAGLSADPYNNWTAWSESDGNGTGQSHHNVFPDCKPFPHPGWRWNIYVFHTL 180

QY 181 GOYFQKLGRCVRSVNTANVTLGQLMVEVYRRHGRAYVPIAQVKDYVVYTDQIPFV 240
DB 181 GOYFQKLGRCVRSVNTANVTLGQLMVEVYRRHGRAYVPIAQVKDYVVYTDQIPFV 240

QY 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPSPFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRNSDETFLKDLPIFMDVLIHDPSPFLNYSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVLNGTFSNLTLTKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
DB 301 HTYVLNGTFSNLTLTKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360

QY 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLDIFVTCQGSIPTEVCTIISDPT 420
DB 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLDIFVTCQGSIPTEVCTIISDPT 420

QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVPDRPAS 480
DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVPDRPAS 480

QY 481 PLRMANSALISVGLAIFFVTYISLLVYKKHKEYNPIENSPGNVVRKSGLSVFLNRAKAVF 540
DB 481 PLRMANSALISVGLAIFFVTYISLLVYKKHKEYNPIENSPGNVVRKSGLSVFLNRAKAVF 540

QY 541 PFGNQEKDPLLNQEFKGVG 560
DB 541 PFGNQEKDPLLNQEFKGVG 560

RESULT 14
ADN39940
ID ADN39940 standard; protein; 560 AA.
XX
XX AC ADN39940;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C310.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnery; gene therapy; vaccine.

XX Homo sapiens.

XX WO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002WO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

XX 29-NOV-2001; 2001US-0334393P.

XX 03-DEC-2001; 2001US-0335393P.

XX 14-DEC-2001; 2001US-0340376P.

XX 08-JAN-2002; 2002US-0347211P.

XX 10-JAN-2002; 2002US-0347343P.

XX 08-FEB-2002; 2002US-0352505P.

XX 13-FEB-2002; 2002US-0356714P.

XX 20-FEB-2002; 2002US-0359077P.

XX 29-MAR-2002; 2002US-0368809P.

XX 04-APR-2002; 2002US-0370110P.

XX 12-APR-2002; 2002US-0372246P.

XX 05-JUN-2002; 2002US-0386614P.

XX 16-JUL-2002; 2002US-0396839P.

XX 22-JUL-2002; 2002US-0397755P.

XX 22-JUL-2002; 2002US-0397845P.

XX 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA; Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A; WPI: 2003-469649/44. N-PSDB; ADN39723.

XX Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C310; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularisation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60

QY 61 VWRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
DB 61 VWRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNNWTAWSEDSGNGTQSHHNVFPDGKPPHPGMRWNFIYVFHTL 180
DB 121 RNEAGLSADPYVYNNWTAWSEDSGNGTQSHHNVFPDGKPPHPGMRWNFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVYVTDQIPVFV 240
DB 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVYVTDQIPVFV 240
QY 241 TMFQKNDNRSSDETFLKDLPIMFVDVLIHDPESHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIMFVDVLIHDPESHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
DB 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
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QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPAS 480
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RESULT 15

ADH56342
ID ADH56342 standard; protein; 560 AA.

AC ADH56342;

DT 25-MAR-2004 (first entry)

DE Human nmb protein SEQ ID NO:1.

KW respiratory disease; human; nmb; antiinflammatory; antiasthmatic;
KW antiallergic; neuroprotective; immunosuppressive; antidiabetic;
KW antiarthritic; dermatological; gastrointestinal; antirheumatic; asthma;
KW hayfever; chronic bronchitis; chronic obstructive lung disease;
KW immune disorder; multiple sclerosis; Sjogren's disease;
KW insulin-resistant diabetes; rheumatoid arthritis; lupus erythematosus;
KW atopic dermatitis; irritable bowel disease.

OS Homo sapiens.

XX WO2004002516-A1.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-JP008168.

XX 28-JUN-2002; 2002JP-00190790.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Nakanishi A, Iwashita H, Morita S, Matsumoto T, Yamasaki M;

XX WPI; 2004-082883/08.

XX N-PSDB; ADH56343.

XX Drug compositions containing inhibitor of human nmb protein activity for

PT treatment and prevention of respiratory diseases including asthma and
PT chronic obstructive lung disease.

PS Claim 1; SEQ ID NO 1; 104pp; Japanese.

XX The present invention describes drug compositions (I) for prevention and
treatment of respiratory diseases, which contain a compound or its salts
inhibiting the activity of human nmb protein or its partial peptides or a
protein of substantially similar sequence and activity, or inhibiting the
expression of the gene encoding this protein. Also described: (1)
antisense polynucleotides to all or part of the nmb gene, and drug
compositions containing them; (2) antibodies to all or part of nmb
(3) diagnostic reagents containing polynucleotides encoding all or part
of nmb protein; (4) screening method for compounds for use in prevention
and treatment of respiratory diseases, using nmb protein or its partial
peptides, or using polynucleotides encoding all or part of nmb protein,
or using a tobacco smoking induced chronic obstructive lung disease model
mouse or an elastase-induced chronic obstructive lung disease model mouse
(5) kits for the screening method; (6) compounds identified by the
screening method; (7) a method for prevention and treatment of
respiratory diseases using the identified compounds; and (8) drug
compositions for prevention and treatment of respiratory diseases
containing a compound or its salts inhibiting the binding activity of
heparan sulfate proteoglycan. (I) have antiinflammatory, antiasthmatic,
antiallergic, neuroprotective, immunosuppressive, antidiabetic,
antiarthritic, dermatological, gastrointestinal, and antirheumatic
activities. (I) can be used for the prevention, treatment and diagnosis
of respiratory diseases such as acute asthma, chronic asthma, hayfever,
chronic bronchitis and chronic obstructive lung disease, and other
diseases including immune disorders such as multiple sclerosis, Sjogren's
disease, insulin-resistant diabetes, rheumatoid arthritis, lupus
erythematosus, atopic dermatitis, and irritable bowel disease. The
present sequence represents human nmb, which is used in the
exemplification of the present invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 8; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 TMFQKNDNRSSDETFLKDLPIMFVDVLIHDPESHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
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DB 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:59:13 ; Search time 147 Seconds

(without alignments)
1349.057 Million cell updates/sec

Title: US-09-853-880A-17

Perfect score: 3026

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Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3026	100.0	560	9	US-09-897-778-225
4	3026	100.0	560	9	US-09-943-075A-6
5	3026	100.0	560	13	US-10-039-272-2
6	3026	100.0	560	14	US-10-007-700-225
7	3026	100.0	560	14	US-10-117-982-225
8	3026	100.0	560	14	US-10-463-106-2
9	3026	100.0	560	14	US-10-295-027-1258
10	3026	100.0	560	14	US-10-313-986-225
11	3026	100.0	560	15	US-10-309-290-152
12	3026	100.0	560	16	US-10-408-765A-466
13	3006	99.3	572	14	US-10-227-884-42

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15	3006	99.3	572	14	US-10-230-338-42	Sequence 42, Appl
16	3006	99.3	572	14	US-10-218-631-42	Sequence 42, Appl
17	3006	99.3	572	14	US-10-230-414-42	Sequence 42, Appl
18	3006	99.3	572	14	US-10-232-224-42	Sequence 42, Appl
19	3006	99.3	572	14	US-10-216-159A-42	Sequence 42, Appl
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21	3006	99.3	572	14	US-10-227-873-42	Sequence 42, Appl
22	3006	99.3	572	14	US-10-227-883-42	Sequence 42, Appl
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24	3006	99.3	572	14	US-10-230-434-42	Sequence 42, Appl
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41	3006	99.3	572	14	US-10-219-470-42	Sequence 42, Appl
42	3006	99.3	572	14	US-10-219-474-42	Sequence 42, Appl
43	3006	99.3	572	14	US-10-219-524-42	Sequence 42, Appl
44	3006	99.3	572	14	US-10-219-528-42	Sequence 42, Appl
45	3006	99.3	572	14	US-10-227-880-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-735-705-225
; Sequence 225, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-705-225

Query Match 100.0%; Score 3026; DB 9; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 225, Application US/09897778			
; Patent No. US20020147143A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Marnerakis, Margarita			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darlick			
; APPLICANT: Watanabe, Yoshihiro			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Peckham, David W.			
; APPLICANT: Fanger, Neil			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; FILE REFERENCE: 210121.455C16			
; CURRENT FILING DATE: 2001-06-28			
; NUMBER OF SEQ ID NOS: 467			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 225			
; LENGTH: 560			
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; ORGANISM: Homo sapiens			
US-09-897-778-225			
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RESULT 4
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; Sequence 6, Application US/09943075A
; Patent No. US20020151486A1
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Faye F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369.262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-943-075A-6

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Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLATSTLSVPRDRPAS 480
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; Sequence 2, Application US/10039272
; Publication No. US20020168653A1
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
; CURRENT APPLICATION NUMBER: US/10/039,272
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272-2

Query Match 100.0%; Score 3026; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Qy 61 VKKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Qy 121 RNEAGLSADPVYVNTWTAWSESDSGENGTCQSHHNVFPDCKRPHHPGWRWNFIYVFTL 180
Db 121 RNEAGLSADPVYVNTWTAWSESDSGENGTCQSHHNVFPDCKRPHHPGWRWNFIYVFTL 180
Qy 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVYVVTQDQIPVF 240
Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVYVVTQDQIPVF 240
Qy 241 TMFQKNDNRSSDETFKDLPIMFEDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDETFKDLPIMFEDVLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Qy 301 HTYVLNGTFSMLNTVKAAPGCPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDP 360
Db 301 HTYVLNGTFSMLNTVKAAPGCPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDP 360
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Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
QY 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTTCGSGIPTVECTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTTCGSGIPTVECTIISDPT 420
QY 421 CEITQNTVCS PVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLISVPDRDPAS 480
Db 421 CEITQNTVCS PVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 PFGNQEKDPLLKNQBFKGV 560
Db 541 PFGNQEKDPLLKNQBFKGV 560

RESULT 6
US-10-007-700-225
; Sequence 225, Application US/10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-225

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVPFDGKPPHPCWRWNFIYVPHLL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVPFDGKPPHPCWRWNFIYVPHLL 180
QY 181 GQYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDIIPVF 240
Db 181 GQYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDIIPVF 240
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QY 241 TMEQKNDRSSDETFLKDLPIIMFDVLIHDPHFNLNYSTINKWSPGDNLTGLFVSTNHTVN 300
Db 241 TMEQKNDRSSDETFLKDLPIIMFDVLIHDPHFNLNYSTINKWSPGDNLTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
QY 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTTCGSGIPTVECTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTTCGSGIPTVECTIISDPT 420
QY 421 CEITQNTVCS PVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLISVPDRDPAS 480
Db 421 CEITQNTVCS PVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 PFGNQEKDPLLKNQBFKGV 560
Db 541 PFGNQEKDPLLKNQBFKGV 560

RESULT 7
US-10-117-982-225
; Sequence 225, Application US/10117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-225

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVPFDGKPPHPCWRWNFIYVPHLL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVPFDGKPPHPCWRWNFIYVPHLL 180
QY 181 GQYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDIIPVF 240
Db 181 GQYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDIIPVF 240
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Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240
QY 241 TMFQKNDNRSSDTEFLKDLPIMFEDVLIHDPHFNLSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDTEFLKDLPIMFEDVLIHDPHFNLSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTVVLNGTSLNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360
Db 301 HTVVLNGTSLNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360
QY 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420
QY 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLGGDDTSLATSTLISVPDRDPAS 480
Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLGGDDTSLATSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 PFGNOEKDPLLNQBFKGV 560
Db 541 PFGNOEKDPLLNQBFKGV 560

RESULT 8
US-10-463-106-2
; Sequence 2, Application US/10463106
; Publication No. US20030202938A1
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-1 GENE
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
; CURRENT APPLICATION NUMBER: US/10/463,106
; CURRENT FILING DATE: 2003-06-17
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 10/039,272
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-463-106-2

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNERPSAYMREHNQNLGWSDDENDWNEKLYP 60
Db 1 MECLYFLGFLLLAARLPDAAKRFHDLGNERPSAYMREHNQNLGWSDDENDWNEKLYP 60
QY 61 VWKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
Db 61 VWKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPVYVNTAWSESDGNGTQSHHNVFDPGKPPHHPGWRWNIYVVEHTL 180
Db 121 RNEAGLSADPVYVNTAWSESDGNGTQSHHNVFDPGKPPHHPGWRWNIYVVEHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240
Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240
QY 241 TMFQKNDNRSSDTEFLKDLPIMFEDVLIHDPHFNLSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDTEFLKDLPIMFEDVLIHDPHFNLSTINYKWSFGDNTGLFVSTNHTVN 300
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QY 301 HTVVLNGTSLNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360
Db 301 HTVVLNGTSLNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360
QY 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420
QY 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLGGDDTSLATSTLISVPDRDPAS 480
Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLGGDDTSLATSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 PFGNOEKDPLLNQBFKGV 560
Db 541 PFGNOEKDPLLNQBFKGV 560

RESULT 9
US-10-295-027-1258
; Sequence 1258, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gieh, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1258
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1258

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
Db	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
QY	61	VKRGDMRKNSWKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIYVEKNC	120
Db	61	VKRGDMRKNSWKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIYVEKNC	120
QY	121	RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVPDGPKPPHHPGWRMNFIVVFHTL	180
Db	121	RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVPDGPKPPHHPGWRMNFIVVFHTL	180
QY	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVVF	240
Db	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVVF	240
QY	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
Db	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
QY	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN	360
Db	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN	360
QY	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
Db	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
QY	421	CEITQNTVCSPVDVDEMCLLTVRRTPNGSGTTCVNLTLGDDTSLALTSLISVDPDRPAS	480
Db	421	CEITQNTVCSPVDVDEMCLLTVRRTPNGSGTTCVNLTLGDDTSLALTSLISVDPDRPAS	480
QY	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF	540
Db	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF	540
QY	541	FPGNQEKDPLLKNQEFKGV	560
Db	541	FPGNQEKDPLLKNQEFKGV	560
RESULT 11			
US-10-309-290-152			
; Sequence 152, Application US/10309290			
; Publication No. US20040023241A1			
; GENERAL INFORMATION:			
; APPLICANT: Alsobrook II, John P.			
; APPLICANT: Anderson, David W.			
; APPLICANT: Boldog, Ferenc L.			
; APPLICANT: Burgess, Catherine E.			
; APPLICANT: Chilikuru, Rajeev A.			
; APPLICANT: Edinger, Shlomit R.			
; APPLICANT: Gerlach, Valerie L.			
; APPLICANT: Gorman, Linda			
; APPLICANT: Gould-Rothberg, Bonnie E.			
; APPLICANT: Guo, Xiaojia			
; APPLICANT: Jeffers, Michael E.			
; APPLICANT: Ji, Weizhen			
; APPLICANT: Li, Li			
; APPLICANT: Malvankar, Uriel M.			
; APPLICANT: Miller, Charles E.			
; APPLICANT: Murphy, Ryan			
; APPLICANT: Patturajan, Meera			
; APPLICANT: Peyman, John A.			
; APPLICANT: Rastelli, Luca			
; APPLICANT: Rieger, Daniel K.			
; APPLICANT: Shenoy, Suresh G.			
; APPLICANT: Smithson, Glennda			
; APPLICANT: Starling, Gary			
; APPLICANT: Taupier, Raymond J.			
; APPLICANT: Voss, Edward Z.			
; APPLICANT: Zhong, Haihong			
; APPLICANT: Zhong, Mei			
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH			
; FILE REFERENCE: 21402-502A			
; CURRENT APPLICATION NUMBER: US/10/309,290			
; CURRENT FILING DATE: 2002-12-02			

QY	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
Db	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
QY	61	VKRGDMRKNSWKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIYVEKNC	120
Db	61	VKRGDMRKNSWKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIYVEKNC	120
QY	121	RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVPDGPKPPHHPGWRMNFIVVFHTL	180
Db	121	RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVPDGPKPPHHPGWRMNFIVVFHTL	180
QY	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVVF	240
Db	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVVF	240
QY	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
Db	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
QY	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN	360
Db	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN	360
QY	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
Db	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
QY	421	CEITQNTVCSPVDVDEMCLLTVRRTPNGSGTTCVNLTLGDDTSLALTSLISVDPDRPAS	480
Db	421	CEITQNTVCSPVDVDEMCLLTVRRTPNGSGTTCVNLTLGDDTSLALTSLISVDPDRPAS	480
QY	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF	540
Db	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF	540
QY	541	FPGNQEKDPLLKNQEFKGV	560
Db	541	FPGNQEKDPLLKNQEFKGV	560
RESULT 10			
US-10-313-986-225			
; Sequence 225, Application US/10313986			
; Publication No. US20030236209A1			
; GENERAL INFORMATION:			
; APPLICANT: FOY, Teresa M.			
; APPLICANT: McNabb, Andria			
; APPLICANT: Watanabe, Yoshihiro			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Wang, Tongtong			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; FILE REFERENCE: 210121.455C19			
; CURRENT APPLICATION NUMBER: US/10/313,986			
; CURRENT FILING DATE: 2002-12-04			
; NUMBER OF SEQ ID NOS: 560			
; SOFTWARE: Fast-Seq for Windows Version 4.0			
; SEQ ID NO 225			
; LENGTH: 560			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-313-986-225			
Query Match 100.0%; Score 3026; DB 14; Length 560;			
Best Local Similarity 100.0%; Pred. No. 3.6e-245;			
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
Db	1	MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60

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/ PRIOR APPLICATION NUMBER: 60/336,600
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: 60/338,285
/ PRIOR FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: 60/341,346
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/341,477
/ PRIOR FILING DATE: 2001-12-17
/ PRIOR APPLICATION NUMBER: 60/341,540
/ PRIOR FILING DATE: 2001-12-17
/ PRIOR APPLICATION NUMBER: 60/342,592
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/344,297
/ PRIOR FILING DATE: 2001-12-27
/ PRIOR APPLICATION NUMBER: 60/344,903
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/373,288
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/380,981
/ PRIOR FILING DATE: 2002-05-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 152
/ LENGTH: 560
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-309-290-152

Query Match      100.0%; Score 3026; DB 15; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MECLYFGLFLLLAARLPDAAKRDHVLGNRPSPAYMREHNLNGWSSDENDMNEKLYP 60
Db      1 MECLYFGLFLLLAARLPDAAKRDHVLGNRPSPAYMREHNLNGWSSDENDMNEKLYP 60

Qy      61 VVKGDMRWKSKWGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
Db      61 VVKGDMRWKSKWGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120

Qy      121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRNRNFIYVHTL 180
Db      121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRNRNFIYVHTL 180

Qy      181 QGYFQKLGRCVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDYYVVTQIPVFV 240
Db      181 QGYFQKLGRCVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDYYVVTQIPVFV 240

Qy      241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPDSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300
Db      241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPDSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300

Qy      301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLSLRIPDENCOIN 360
Db      301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLSLRIPDENCOIN 360

Qy      361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTEVCITIIISDPT 420
Db      361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTEVCITIIISDPT 420

Qy      421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTLSTLISVDPDRPAS 480
Db      421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTLSTLISVDPDRPAS 480

Qy      481 PLRMANSALISVGCLAIFTVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
Db      481 PLRMANSALISVGCLAIFTVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540

Qy      541 FPGNQEKDPLLNKQEFKGV 560
Db      541 FPGNQEKDPLLNKQEFKGV 560
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RESULT 13
US-10-227-884-42

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RESULT 12
US-10-408-765A-466
/ Sequence 466, Application US/10408765A
/ Publication No. US20040101874A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Soumitra S.
/ APPLICANT: Fahy, Boin D.
/ APPLICANT: Zhang, Bing
/ APPLICANT: Gibson, Bradford W.
/ APPLICANT: Taylor, Steven W.
/ APPLICANT: Glenn, Gary M.
/ APPLICANT: Warnock, Dale E.
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
/ FILE REFERENCE: 660088.465
/ CURRENT APPLICATION NUMBER: US/10/408,765A
/ CURRENT FILING DATE: 2003-04-04
/ NUMBER OF SEQ ID NOS: 3077
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 466
/ LENGTH: 560
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-408-765A-466
```

```
Query Match      100.0%; Score 3026; DB 16; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MECLYFGLFLLLAARLPDAAKRDHVLGNRPSPAYMREHNLNGWSSDENDMNEKLYP 60
Db      1 MECLYFGLFLLLAARLPDAAKRDHVLGNRPSPAYMREHNLNGWSSDENDMNEKLYP 60

Qy      61 VVKGDMRWKSKWGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
Db      61 VVKGDMRWKSKWGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120

Qy      121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRNRNFIYVHTL 180
Db      121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRNRNFIYVHTL 180

Qy      181 QGYFQKLGRCVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDYYVVTQIPVFV 240
Db      181 QGYFQKLGRCVRVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDYYVVTQIPVFV 240

Qy      241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPDSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300
Db      241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPDSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300

Qy      301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLSLRIPDENCOIN 360
Db      301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLSLRIPDENCOIN 360

Qy      361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTEVCITIIISDPT 420
Db      361 RYGHFQATITIVEGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTEVCITIIISDPT 420

Qy      421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTLSTLISVDPDRPAS 480
Db      421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTLSTLISVDPDRPAS 480

Qy      481 PLRMANSALISVGCLAIFTVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
Db      481 PLRMANSALISVGCLAIFTVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540

Qy      541 FPGNQEKDPLLNKQEFKGV 560
Db      541 FPGNQEKDPLLNKQEFKGV 560
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Sequence 42, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
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PRIOR APPLICATION NUMBER: 60/099816
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PRIOR FILING DATE: 1998-09-11
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PRIOR APPLICATION NUMBER: 60/106178
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PRIOR APPLICATION NUMBER: 60/106248
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PRIOR APPLICATION NUMBER: 60/106464
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PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
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PRIOR FILING DATE: 1998-11-18
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PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
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; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
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;
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
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; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
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; PRIOR APPLICATION NUMBER: 60/113296
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; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
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; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
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; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
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; PRIOR APPLICATION NUMBER: 60/144758
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; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733

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; PRIORITY FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: 60/164418
; PRIORITY FILING DATE: 1999-11-09
; PRIORITY APPLICATION NUMBER: 60/166361
; PRIORITY FILING DATE: 1999-11-16
; PRIORITY APPLICATION NUMBER: 60/169445
; PRIORITY FILING DATE: 1999-12-07
; PRIORITY APPLICATION NUMBER: 60/169495
; PRIORITY FILING DATE: 1999-12-07
; PRIORITY APPLICATION NUMBER: 60/169835

Query Match
Best Local Similarity 99.3%; Score 3006; DB 14; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFGLFLLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MECLYFGLFLLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIYVEKNC 120
DB 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNNTAWSESDGNGTQSHHNVFPDGPFPHPGWRWNFIYVFHTL 180
DB 121 RNEAGLSADPYVYNNTAWSESDGNGTQSHHNVFPDGPFPHPGWRWNFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQDIPVFV 240
DB 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQDIPVFV 240
QY 241 TMFQKNDNRSSDETFLKDLPIPMFDVLIHDPESHFLVNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIPMFDVLIHDPESHFLVNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSLTLKSYDSNTGPTGDNPLE 360
QY 349 LSRIPEQNCINRYGHQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVVTQCGSI 408
DB 361 LSRIPEQNCINRYGHQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVVTQCGSI 420
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCVNLTGDDTSLALTS 468
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCVNLTGDDTSLALTS 480
QY 469 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 528
DB 481 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 540
QY 529 LSVFLNRAKAVFFPGNOEKDPLLNQKQEPKGV 560
DB 541 LSVFLNRAKAVFFPGNOEKDPLLNQKQEPKGV 572

RESULT 15
US-10-230-338-42
; Sequence 42, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIORITY APPLICATION NUMBER: 10/119,480
; PRIORITY FILING DATE: 2002-04-09
; PRIORITY APPLICATION NUMBER: 60/059113
; PRIORITY FILING DATE: 1997-09-17
; PRIORITY APPLICATION NUMBER: 60/062287
; PRIORITY FILING DATE: 1997-10-17
; PRIORITY APPLICATION NUMBER: 60/063549
; PRIORITY FILING DATE: 1997-10-28
; PRIORITY APPLICATION NUMBER: 60/064103
; PRIORITY FILING DATE: 1997-10-31
; PRIORITY APPLICATION NUMBER: 60/069873
; PRIORITY FILING DATE: 1997-12-17
; PRIORITY APPLICATION NUMBER: 60/078910
; PRIORITY FILING DATE: 1998-03-20
; PRIORITY APPLICATION NUMBER: 60/079294
; PRIORITY FILING DATE: 1998-03-25
; PRIORITY APPLICATION NUMBER: 60/079656
; PRIORITY FILING DATE: 1998-03-26
; PRIORITY APPLICATION NUMBER: 60/079728
; PRIORITY FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 42
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-230-338-42
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Query Match
Best Local Similarity 99.3%; Score 3006; DB 14; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFGLFLLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MECLYFGLFLLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIYVEKNC 120
DB 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNNTAWSESDGNGTQSHHNVFPDGPFPHPGWRWNFIYVFHTL 180
DB 121 RNEAGLSADPYVYNNTAWSESDGNGTQSHHNVFPDGPFPHPGWRWNFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQDIPVFV 240
DB 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQDIPVFV 240
QY 241 TMFQKNDNRSSDETFLKDLPIPMFDVLIHDPESHFLVNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIPMFDVLIHDPESHFLVNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSLTLKSYDSNTGPTGDNPLE 360
QY 349 LSRIPEQNCINRYGHQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVVTQCGSI 408
DB 361 LSRIPEQNCINRYGHQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVVTQCGSI 420
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCVNLTGDDTSLALTS 468
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCVNLTGDDTSLALTS 480
QY 469 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 528
DB 481 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 540
QY 529 LSVFLNRAKAVFFPGNOEKDPLLNQKQEPKGV 560
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Db 541 USVFLNRAKAVFFPGNQERDPLLLKNQEFKGS 572

Search completed: November 19, 2004, 15:11:31
Job time : 150 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:42:06 ; Search time 199 Seconds
(without alignments)
1619.145 Million cell updates/sec

Title: US-09-853-880A-17
Perfect score: 3026
Sequence: 1 MECLYFLGLLLAARLPD.....PFGNQKDPLLKNQEPKGVGS 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3026	100.0	560	1	NMB_HUMAN	Q14956 homo sapien
2	3026	100.0	560	2	AAP22336	Aap22336 homo sapi
3	3010	99.5	572	2	Q8N1A1	Q8N1A1 homo sapien
4	3006	99.3	572	2	Q8UVX1	Q8UVX1 homo sapien
5	3006	99.3	572	2	AAQ89481	AAQ89481 homo sapi
6	2197	72.6	574	2	Q8BVV9	Q8BVV9 mus musculu
7	2197	72.6	574	2	Q9QXA0	Q9QXA0 mus musculu
8	2197	72.6	574	2	Q99P91	Q99P91 mus musculu
9	2193	72.5	574	2	Q8BXL4	Q8BXL4 mus musculu
10	2179	72.0	572	2	Q8P7C7	Q8P7C7 rattus norv
11	2179	72.0	572	2	AAH61725	AAH61725 rattus nor
12	2163	71.5	572	2	Q9QZP6	Q9QZP6 rattus norv
13	2042	67.5	526	2	Q8BVA0	Q8BVA0 mus musculu
14	1588.5	52.5	559	1	QNR_COTJA	Q90372 coturnix co
15	1029	34.0	206	2	Q96F58	Q96F58 homo sapien
16	1022	33.8	206	2	Q8IXJ5	Q8IXJ5 homo sapien
17	736.5	24.3	721	2	Q6DDN6	Q6DDN6 xenopus lae
18	729.5	24.1	746	2	Q6DIR2	Q6DIR2 xenopus tro
19	671.5	22.2	626	2	Q9CZB2	Q9CZB2 mus musculu
20	659	21.8	626	1	PM17_MOUSE	Q60696 mus musculu
21	653.5	21.6	760	2	Q6DW64	Q6DW64 gallus gall
22	651	21.5	733	2	Q93391	Q93391 coturnix co
23	651	21.5	733	2	AA82576	AA82576 coturnix
24	650.5	21.5	764	2	Q6DW63	Q6DW63 gallus gall
25	650	21.5	763	2	Q6DW62	Q6DW62 gallus gall
26	642.5	21.2	788	2	Q6DW65	Q6DW65 gallus gall
27	639	21.1	762	1	P115_CHICK	Q98917 gallus gall
28	634	21.0	783	2	Q6DW60	Q6DW60 gallus gall
29	631	20.9	759	2	Q6DW61	Q6DW61 gallus gall
30	622	20.6	661	1	PM17_HUMAN	P40967 homo sapien
31	622	20.6	661	2	AAP35866	Aap35866 homo sapi

32 459 15.2 491 1 PM17_BOVIN
33 399 13.2 461 2 Q97884
34 247.5 8.2 236 2 Q9QY67
35 182 6.0 397 2 Q8N3R2
36 181.5 6.0 423 2 Q8N0W9
37 181.5 6.0 423 2 AAQ88946
38 181 6.0 435 2 Q8N3G9
39 167 5.5 141 2 Q9QY70
40 156 5.2 419 2 Q6NXM3
41 155 5.2 419 2 AAH67004
42 155.5 5.1 354 2 Q8IY46
43 144 4.8 3988 2 Q8TPZ1
44 142.5 4.7 1817 2 Q8TI59
45 140 4.6 688 2 Q8TR88

ALIGNMENTS

RESULT 1
NMB_HUMAN
ID NMB_HUMAN STANDARD; PRT; 560 AA.
AC Q14956;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative transmembrane protein NMB precursor (Transmembrane
glycoprotein HGFIN).
GN Name=GNMNB; Synonyms=NMB, HGFIN;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95113576; PubMed=7814155;
RA Wettersman M.A.J., Ajubi N., van Dinter I.M.R., Degen W.G.J.,
van Muijen G.N.P., Ruiter D.J., Bloemers H.P.J.;
RT "NMB, a novel gene, is expressed in low-metastatic human melanoma cell
lines and xenografts.";
RL Int. J. Cancer 60:73-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=22498106; PubMed=12609765;
RA Bandari P.S., Qian J., Yehia G., Joshi D.D., Maloof P.B., Potian J.,
Oh H.S., Gascon P., Harrison J.S., Rameshwar P.;
RT "Hematopoietic growth factor inducible neurokinin-1 type: a
transmembrane protein that is similar to neurokinin 1 interacts with
substance P.";
RL Regul. Pept. 111:169-178(2003).
CC -!- FUNCTION: Could be a melanogenic enzyme (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Not restricted to the melanocytic lineage.
CC -!- DEVELOPMENTAL STAGE: Expression in poorly metastatic melanoma cell
lines; no expression in highly metastatic melanoma cell lines.
CC -!- SIMILARITY: Belongs to the Pmel-17/NMB family.
CC -!- SIMILARITY: Contains 1 PKD domain.

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EMBL; X76534; CAA54044.1; -.
EMBL; AF322909; AAG42839.1; -.
PIR; I38065; I38065.
Genew; HGNC:4462; GPNMB.
MIM; 604368; -.

DR GO:0016021; C: integral to membrane; TAS.
DR GO:0008285; P: negative regulation of cell proliferation; TAS.
DR InterPro: IPR000601; PKD.
DR Pfam: PF00801; PKD; 1.
DR PROSITE: PS00933; PKD; 1.
KW Glycoprotein; Polymorphism; Signal, Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 560
FT DOMAIN 22 486
FT TRANSMEM 487 507
FT DOMAIN 508 560
FT DOMAIN 240 327
FT DOMAIN 320 332
FT CARBOHYD 93 93
FT CARBOHYD 134 134
FT CARBOHYD 146 146
FT CARBOHYD 200 200
FT CARBOHYD 249 249
FT CARBOHYD 275 275
FT CARBOHYD 296 296
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 312 312
FT CARBOHYD 447 447
FT CARBOHYD 455 455
FT VARIANT 195 195
FT VARIANT 197 197
FT FTID=VAR 012076.
FT N -> H (in dbSNP:530413).
FT FTID=VAR 012077.
SEQUENCE 560 AA; 62643 MW; 570035B48CCE3ECC CRC64;
Query Match 100.0%; Score 3026; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.5e-218;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERPSPAYMRHNLNGWSSDENDWNEKLYP 60
DB 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERPSPAYMRHNLNGWSSDENDWNEKLYP 60
QY 61 VKRGMWKNKSKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
DB 61 VKRGMWKNKSKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSDESGENGTSQSHNVFPDGPFPHPGWRWNFIYVFTL 180
DB 121 RNEAGLSADPYVYNWTAWSDESGENGTSQSHNVFPDGPFPHPGWRWNFIYVFTL 180
QY 181 GOYFQKLGRCVRSVNTANTVILGPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240
DB 181 GOYFQKLGRCVRSVNTANTVILGPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240
QY 241 TMFQKNDNRNSDDETFLLKDLPIMFVLIHDSHFLNYSNTINYSKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRNSDDETFLLKDLPIMFVLIHDSHFLNYSNTINYSKWSFGDNTGLFVSTNHTVN 300
QY 301 HTVVLNGTFSNLTVKAAAGPCPPPPPPPPPPPPPPPSLPGAGNPLELSRIPENCQIN 360
DB 301 HTVVLNGTFSNLTVKAAAGPCPPPPPPPPPPPPPPPSLPGAGNPLELSRIPENCQIN 360
QY 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSIPTVEVCTIISDPT 420
DB 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLIIDFVTCQSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSFVDVDECLLTVTRTFNGSGTYCNVLTGLDDTSLALTSLISVDPDRPAS 480
DB 421 CEITQNTVCSFVDVDECLLTVTRTFNGSGTYCNVLTGLDDTSLALTSLISVDPDRPAS 480
QY 481 PLRWANSLISVGCIAIFVTVISLLVYKKHKEYNPNIENSPGNVRSKGLSVFLNRAKAVF 540
DB 481 PLRWANSLISVGCIAIFVTVISLLVYKKHKEYNPNIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLNQEFKGV 560

Db 541 FPGNQEKDPLLNQEFKGV 560
RESULT 2
AAP22336 PRELIMINARY; PRT; 560 AA.
AC AAP22336;
DT 02-WAR-2004 (TREMELrel. 27, Created)
DT 02-WAR-2004 (TREMELrel. 27, Last sequence update)
DE 02-WAR-2004 (TREMELrel. 27, Last annotation update)
DE Hypothetical protein GPNMB.
GN GPNMB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RX MEDLINE=99063792; PubMed=9847074;
RP SEQUENCE FROM N.A.
RA Wilson R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Kalicki J., Kramer J.;
RT "The sequence of Homo sapiens BAC clone CTA-271G13.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005082; AAP22336.1; -.
KW Hypothetical protein.
SQ SEQUENCE 560 AA; 62643 MW; 570035B48CCE3ECC CRC64;
Query Match 100.0%; Score 3026; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.5e-218;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERPSPAYMRHNLNGWSSDENDWNEKLYP 60
DB 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERPSPAYMRHNLNGWSSDENDWNEKLYP 60
QY 61 VKRGMWKNKSKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
DB 61 VKRGMWKNKSKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSDESGENGTSQSHNVFPDGPFPHPGWRWNFIYVFTL 180
DB 121 RNEAGLSADPYVYNWTAWSDESGENGTSQSHNVFPDGPFPHPGWRWNFIYVFTL 180
QY 181 GOYFQKLGRCVRSVNTANTVILGPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240
DB 181 GOYFQKLGRCVRSVNTANTVILGPQLMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240
QY 241 TMFQKNDNRNSDDETFLLKDLPIMFVLIHDSHFLNYSNTINYSKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRNSDDETFLLKDLPIMFVLIHDSHFLNYSNTINYSKWSFGDNTGLFVSTNHTVN 300

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Db      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLNSTYINXKWSFGDNTGLFVSTNHTVN 300
QY      301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTSPSLGPDGNDPLELSRIPDNCQIN 360
Db      301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTSPSLGPDGNDPLELSRIPDNCQIN 360
QY      361 RYGHFOQATITIVGILEVNIQMTDVLMPVMPPESSLDIFVVTCCGSIPTVECTIISOPT 420
Db      361 RYGHFOQATITIVGILEVNIQMTDVLMPVMPPESSLDIFVVTCCGSIPTVECTIISOPT 420
QY      421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDDTSLAITSRLISVPRDRPAS 480
Db      421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDDTSLAITSRLISVPRDRPAS 480
QY      481 PLRMANSALISVGCLAIFFVTIVSLVYKHKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db      481 PLRMANSALISVGCLAIFFVTIVSLVYKHKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
QY      541 FPGNQEKDPLLNQKQEPFGVS 560
Db      541 FPGNQEKDPLLNQKQEPFGVS 560

RESULT 3
Q8N1A1
ID Q8N1A1 PRELIMINARY; PRT; 572 AA.
AC Q8N1A1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GPNMB protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032783; AAH32783.1; -
DR InterPro; IPR000601; PKD.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS50093; PKD; 1.
SQ SEQUENCE 572 AA; 63922 MW; 2465C12C2F0F3996 CRC64;

Query Match 99.5%; Score 3010; DB 2; Length 572;
Best Local Similarity 97.9%; Pred. No. 4.1e-217;
Matches 560; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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QY      1 MECLYFFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMRHNLQAGWSSDENDWNEKLYP 60
Db      1 MECLYFFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMRHNLQAGWSSDENDWNEKLYP 60
QY      61 VWKRGDMWKNSWKGRVQAVLITSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
Db      61 VWKRGDMWKNSWKGRVQAVLITSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
QY      121 RNEAGLSADPYVYNWTAMSESDSGENGTCQSHHNVFPDGPHPHGRWRWNFIYVFHTL 180
Db      121 RNEAGLSADPYVYNWTAMSESDSGENGTCQSHHNVFPDGPHPHGRWRWNFIYVFHTL 180
QY      181 GQYFQKLGRCSVRVSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDQVYVVDQIPVFV 240
Db      181 GQYFQKLGRCSVRVSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDQVYVVDQIPVFV 240
QY      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLNSTYINXKWSFGDNTGLFVSTNHTVN 300
Db      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLNSTYINXKWSFGDNTGLFVSTNHTVN 300
QY      301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTSPSL-----GPAGDNPLE 348
Db      301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTSPSLATLTKSYDNTTGPAGDNPLE 360
QY      349 LSRIPDENCQINRYGHFOQATITIVGILEVNIQMTDVLMPVMPPESSLDIFVVTCCGSI 408
Db      361 LSRIPDENCQINRYGHFOQATITIVGILEVNIQMTDVLMPVMPPESSLDIFVVTCCGSI 420
QY      409 PTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDDTSLAITS 468
Db      421 PTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDDTSLAITS 480
QY      469 TLISVPRDRPASPLRMANSALISVGCLAIFFVTIVSLVYKHKHKEYNPIENSPGNVRSK 528
Db      481 TLISVPRDRPASPLRMANSALISVGCLAIFFVTIVSLVYKHKHKEYNPIENSPGNVRSK 540
QY      529 LSVFLNRAKAVFFPGNQEKDPLLNQKQEPFGVS 560
Db      541 LSVFLNRAKAVFFPGNQEKDPLLNQKQEPFGVS 572

RESULT 4
Q6UVX1
ID Q6UVX1 PRELIMINARY; PRT; 572 AA.
AC Q6UVX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NMB.
GN ORFNames=UNQ1725;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RT Genome Res. 13:2265-2270 (2003).
DR EMBL; AY359124; AAQ89481.1; -.
DR InterPro; IPR000601; PKD.

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DR SMART; SM00089; PKD; 1.
DR PROSITE; P55093; PKD; 1.
SQ SEQUENCE 572 AA; 63952 MW; D8C20E0499C018CE CRC64;

Query Match
Best Local Similarity 99.3%; Score 3006; DB 2; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNLQNGWSDDNDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNLQNGWSDDNDWNEKLYP 60
QY 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVYKNC 120
DB 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVYKNC 120
QY 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRMNFYVVFHTL 180
DB 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRMNFYVVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVVVTVDQIPV 240
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVVVTVDQIPV 240
QY 241 TMFQKNDNRSSDETFLKDLPIMFVLIHDPSPHFLNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIMFVLIHDPSPHFLNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
QY 349 LSRIPDENCQINRYGHFOATITIVGILEVNIITQMTDVLMPVPWPSSLIIDFVTCQSSI 408
DB 349 LSRIPDENCQINRYGHFOATITIVGILEVNIITQMTDVLMPVPWPSSLIIDFVTCQSSI 408
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
DB 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
QY 469 TLISVDPDRPASPLRMANSALISVGCLAIFFVTVISLLVYKKHKEYNPIENSPGNVRSKG 528
DB 469 TLISVDPDRPASPLRMANSALISVGCLAIFFVTVISLLVYKKHKEYNPIENSPGNVRSKG 528
QY 529 LSVFLNRKAVPFPNGQEKDPLLNQEFKGV 560
DB 541 LSVFLNRKAVPFPNGQEKDPLLNQEFKGV 572

RESULT 5

AAQ89481 ID AAQ89481 PRELIMINARY; PRT; 572 AA.
AC AAQ89481
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE NMB.
GN UNQ1725.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble B., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY359124; AAQ89481.1; -.
SQ SEQUENCE 572 AA; 63952 MW; D8C20E0499C018CE CRC64;

Query Match
Best Local Similarity 99.3%; Score 3006; DB 2; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNLQNGWSDDNDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNLQNGWSDDNDWNEKLYP 60
QY 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVYKNC 120
DB 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVYKNC 120
QY 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRMNFYVVFHTL 180
DB 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRMNFYVVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVVVTVDQIPV 240
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVVVTVDQIPV 240
QY 241 TMFQKNDNRSSDETFLKDLPIMFVLIHDPSPHFLNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIMFVLIHDPSPHFLNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
QY 349 LSRIPDENCQINRYGHFOATITIVGILEVNIITQMTDVLMPVPWPSSLIIDFVTCQSSI 408
DB 349 LSRIPDENCQINRYGHFOATITIVGILEVNIITQMTDVLMPVPWPSSLIIDFVTCQSSI 408
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
DB 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
QY 469 TLISVDPDRPASPLRMANSALISVGCLAIFFVTVISLLVYKKHKEYNPIENSPGNVRSKG 528
DB 469 TLISVDPDRPASPLRMANSALISVGCLAIFFVTVISLLVYKKHKEYNPIENSPGNVRSKG 528
QY 529 LSVFLNRKAVPFPNGQEKDPLLNQEFKGV 560
DB 541 LSVFLNRKAVPFPNGQEKDPLLNQEFKGV 572

RESULT 6

Q8BVV9 ID Q8BVV9 PRELIMINARY; PRT; 574 AA.
AC Q8BVV9
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732452017 product:glycoprotein (transmembrane) nmb,
DE full insert sequence.
GN Name=Gpmmb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;


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SQ SEQUENCE 574 AA; 63691 MW; E0759D7625F0829A CRC64;
Query Match 72.6%; Score 2197; DB 2; Length 574;
Best Local Similarity 70.7%; Pred. No. 3.9e-156;
Matches 403; Conservative 69; Mismatches 82; Indels 16; Gaps 2;

QY 1 MECLYFGLFLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSWSDNDWNEKLYP 60
DB 1 MESLGGVLGLAAGLPDAAKRFHDVILGNRPSAYMREHNLQNGSWSDNDWNEHLYP 60
QY 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFVNLVPRCQKEDANGNIYVKNC 120
DB 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFVNLVPRCQKEDANGNIYVKNC 120
QY 121 RNEAGLSADPYVYNWTAWSDESDGNGTQSHHNVFPDGGKPPHFGWRNFIYVPHTL 180
DB 121 RNDLGLTSLHVNWTAGADGDWEDGTSRSHLRFPDRPPRPHGKWKSVYVPHTL 180
QY 181 GQYFQKLGRCVRSVNTANVTLPOLMEVTVYRRHGRAVPIAOKVYVVDQIPVFV 240
DB 181 GQYFQKLGRCVRSVNTANVTLPOLMEVTVYRRHGRAVPIAOKVYVVDQIPVFV 240
QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLHDPSSHFLNVTSTNYKWSFGDNTGLFVSTHVN 300
DB 241 TMSQKNDNRNLSDFIPLDPIFMDVLHDPSSHFLNVTSTNYKWSFGDNTGLFVSTHVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGPCP-----PPPPPPPP-----SKPTPSLGPAGD 344
DB 301 HTYVLNGTFSNLTVKAAAPGPCP-----PPPPPPPP-----SKPTPSLGPAGD 344
QY 345 NPELSRIPDENCQINRYGHQATITIVGILEVNIQMDVLMVPWPPESSILDFVVC 404
DB 345 NPELSRIPDENCQINRYGHQATITIVGILEVNIQMDVLMVPWPPESSILDFVVC 404
QY 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMPPTQPANSIMDFVTVC 420
DB 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMPPTQPANSIMDFVTVC 420
QY 405 QGSIPTVEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRFTNGSGTGYCNVLTGDDTSL 464
DB 405 QGSIPTVEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRFTNGSGTGYCNVLTGDDTSL 464
QY 421 KGATPMEACTIISDPTCQIAQNRVCSFVAVDGLCLLSVRRAFNGSGTGYCNVLTGDDASL 480
DB 421 KGATPMEACTIISDPTCQIAQNRVCSFVAVDGLCLLSVRRAFNGSGTGYCNVLTGDDASL 480

RESULT 8
Q99P91 PRELIMINARY; PRT; 574 AA.
AC 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dendritic cell-associated transmembrane protein (Glycoprotein
DE (Transmembrane) nmb)
GN Name=Gpmmb; Synonym=Dchl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Shikano S., Bonkobara M., Zukas P.K., Ariizumi K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322054; AAK14240.1; -.
DR EMBL; BC026375; AAK26375.1; -.
DR MGI; MGI:1934765; Gpmmb.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0008201; F:heparin binding; IDA.
DR GO; GO:0005178; F:integrin binding; IDA.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR000583; GATase_2.
DR InterPro; IPR000601; PKD.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
DR PROSITE; PS00093; PKD; 1.
DR Transmembrane.
KW SEQUENCE 574 AA; 63674 MW; B6AE9AC27AE6ACD0 CRC64;
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Query Match 72.6%; Score 2197; DB 2; Length 574;
Best Local Similarity 70.7%; Pred. No. 3.9e-156;
Matches 403; Conservative 69; Mismatches 82; Indels 16; Gaps 2;

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QY 1 MECLYFGLFLAARLPDAAKRFHDVILGNRPSAYMREHNLQNGSWSDNDWNEKLYP 60
DB 1 MESLGGVLGLAAGLPDAAKRFHDVILGNRPSAYMREHNLQNGSWSDNDWNEHLYP 60
QY 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFVNLVPRCQKEDANGNIYVKNC 120
DB 61 VMKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFVNLVPRCQKEDANGNIYVKNC 120
QY 121 RNEAGLSADPYVYNWTAWSDESDGNGTQSHHNVFPDGGKPPHFGWRNFIYVPHTL 180
DB 121 RNDLGLTSLHVNWTAGADGDWEDGTSRSHLRFPDRPPRPHGKWKSVYVPHTL 180
QY 181 GQYFQKLGRCVRSVNTANVTLPOLMEVTVYRRHGRAVPIAOKVYVVDQIPVFV 240
DB 181 GQYFQKLGRCVRSVNTANVTLPOLMEVTVYRRHGRAVPIAOKVYVVDQIPVFV 240
QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLHDPSSHFLNVTSTNYKWSFGDNTGLFVSTHVN 300
DB 241 TMSQKNDNRNLSDFIPLDPIFMDVLHDPSSHFLNVTSTNYKWSFGDNTGLFVSTHVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGPCP-----PPPPPPPP-----SKPTPSLGPAGD 344
DB 301 HTYVLNGTFSNLTVKAAAPGPCP-----PPPPPPPP-----SKPTPSLGPAGD 344
QY 345 NPELSRIPDENCQINRYGHQATITIVGILEVNIQMDVLMVPWPPESSILDFVVC 404
DB 345 NPELSRIPDENCQINRYGHQATITIVGILEVNIQMDVLMVPWPPESSILDFVVC 404
QY 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMPPTQPANSIMDFVTVC 420
DB 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMPPTQPANSIMDFVTVC 420
QY 405 QGSIPTVEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRFTNGSGTGYCNVLTGDDTSL 464
DB 405 QGSIPTVEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRFTNGSGTGYCNVLTGDDTSL 464
QY 421 KGATPMEACTIISDPTCQIAQNRVCSFVAVDGLCLLSVRRAFNGSGTGYCNVLTGDDASL 480
DB 421 KGATPMEACTIISDPTCQIAQNRVCSFVAVDGLCLLSVRRAFNGSGTGYCNVLTGDDASL 480
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Db      61  VWRGEGRWKSWEGRGVQAALTSDSPALVGSNITFVNLFVRCQKEDANGNIVYERN 120
      121  RNEAGLSADPYVYNTWTAMSEDSGNGTQSHHNVPDGKPPPHGWRWNFIYVFHTL 180
      121  RSDLELASDPYVYNTWTGADDEWEDSTSQGHLRFDPGKPPRPHGRKKWFIYVFHTL 180
      181  GQYFQKLGRCSVRSVNTANVTLGPOLMEVTVYRRHGRAYPIAQVKDYVYVTDQIPVF 240
      181  GQYFQKLGRC SARVSINTVNLTVGPQVMEVIVERRHGRAYIPISKVKDYVYVTDQIPVF 240
      241  TMFQKNDNRSSDETFLKOLPIFEDVLHDPSPFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      241  TMVQKNDNRSSDETFLRDLPIFDVLHDPSPFLNYSAISKWNFGDNTGLFVSNHNTLN 300
      301  HTYVLNGTFSNLITVKAAPGCPPPPPPPRP-----SKTPSLGPAGDNP 346
      301  HTYVLNGTFNLTQTAVPGCPSPTPSPSSSTSPSPASSPSTLSTPSPSLMPTGHKS 360
      347  LELSRIPDENCOINRYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLDFVVTGCG 406
      361  MELSDISNENCRINRYGYFRATITIVDGLILEVNIQVADVPIPTPODNLMDFIYVTCG 420
      407  SIPTVECTIISDPTCEITONTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLAL 466
      421  APTTEACTIISDPTCQIAQNRVCSVAVDELCLLSVRRAFNGSGTYCVNFTLGDDASLAL 480
      467  TSTLSVPRDRPASPLRMANSALISVGCLAIPTVTVISLVYKKHKEYNPIENSPGNVRS 526
      481  TSALISIFGKDLGSLRTVNGVLISIGCLAMFVTMTLLYKKHKEYPIGNCTRNWVK 540
      527  KGLSVFLNRKAVFPFGNCKDPLLNQ 554
      541  KGLSVFLSHAKAPFSGRGDREKDLPLQDK 568

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RESULT 12

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Q9QZF6 ID Q9QZF6 PRELIMINARY; PRT; 572 AA.
AC Q9QZF6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Osteoactivin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RX MEDLINE=21611396; PubMed=11746512;
RA Safadi F.F., Xu J., Smock S.L., Rico M.C., Owen T.A., Popoff S.N.;
RT "Cloning and characterization of osteoactivin, a novel cDNA expressed
in osteoblasts."
RL J. Cell. Biochem. 84:12-26(2001).
[2]
RP SEQUENCE FROM N.A.
RA Odgren P.R., Marks S.C. Jr.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Xu J., Safadi F.F., Rosenzweig A.B., Popoff S.N.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184983; AAF03400.1; -.
DR InterPro; IPR000601; PKD.
DR SMART; SMO0089; PKD; 1.
DR PROSITE; PS00093; PKD; 1.
SQ SEQUENCE 572 AA; 63772 MW; CB939F043EC57EB CRC64;

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Query Match

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Best Local Similarity 71.5%; Score 2163; DB 2; Length 572;
Matches 394; Conservative 75; Mismatches 85; Indels 14; Gaps 1;

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QY      1  MECLYYFLGLLLAARLPDAAKRPHDVLGNRPSPAYMRHNLQNGSSDENDWNKLYP 60
      1  MESLCGLVFLLLAAGLPQAAKRPRDLVGHQYPDHMRNNQLRCGSSDENEDWDLQLYP 60
      61  VMKRGDMRWKNSKWKGRVQAALTSDSPALVGSNITFVNLIIPRCQKEDANGNIVYERN 120
      61  VMRRGEGRWKDSWEGRGVQAALTSDSPALVGSNITFVNLIIPRCQKEDANGNIVYERN 120
      121  RNEAGLSADPYVYNTWTAMSEDSGNGTQSHHNVPDGKPPPHGWRWNFIYVFHTL 180
      121  RSDLELASDPYVYNTWTGADDEWEDSTSQGHLRFDPGKPPRPHGRKKWFIYVFHTL 180
      181  GQYFQKLGRC SVRSVNTANVTLGPOLMEVTVYRRHGRAYPIAQVKDYVYVTDQIPVF 240
      181  GQYFQKLGRC SARVSINTVNLTVGPQVMEVIVERRHGRAYIPISKVKDYVYVTDQIPVF 240
      241  TMFQKNDNRSSDETFLKOLPIFEDVLHDPSPFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      241  TMVQKNDNRSSDETFLRDLPIFDVLHDPSPFLNYSAISKWNFGDNTGLFVSNHNTLN 300
      301  HTYVLNGTFSNLITVKAAPGCPPPPPPPRP-----SKTPSLGPAGDNP 346
      301  HTYVLNGTFNLTQTAVPGCPSPTPSPSSSTSPSPASSPSTLSTPSPSLMPTGHKS 360
      347  LELSRIPDENCOINRYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLDFVVTGCG 406
      361  MELSDISNENCRINRYGYFRATITIVDGLILEVNIQVADVPIPTPODNLMDFIYVTCG 420
      407  SIPTVECTIISDPTCEITONTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLAL 466
      421  APTTEACTIISDPTCQIAQNRVCSVAVDELCLLSVRRAFNGSGTYCVNFTLGDDASLAL 480
      467  TSTLSVPRDRPASPLRMANSALISVGCLAIPTVTVISLVYKKHKEYNPIENSPGNVRS 526
      481  TSALISIFGKDLGSLRTVNGVLISIGCLAMFVTMTLLYKKHKEYPIGNCTRNWVK 540
      527  KGLSVFLNRKAVFPFGNCKDPLLNQ 554
      541  KGLSVFLSHAKAPFSGRGDREKDLPLQDK 568

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RESULT 13

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Q8BVA0 ID Q8BVA0 PRELIMINARY; PRT; 526 AA.
AC Q8BVA0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:9530038P20 product:glycoprotein
DE (transmembrane) nmb, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA The FANTOM Consortium,

```

the RIKEN Genome Exploration Research Group Phase I & II Team;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573 (2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 Genome Res. 10:1617-1630 (2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771 (2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kondo S., Konno H., Kouda M., Koya S.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saiboh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK079220; BAC37578.1;
 DR GO; GO:0016021; C-integral to membrane; IEA.
 DR InterPro; IPR000583; GATase_2.
 DR InterPro; IPR000601; PKD.
 DR SMART; SM00089; PKD; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
 DR PROSITE; PS50093; PKD; 1.
 KW Transmembrane.
 SQ SEQUENCE 526 AA; 58250 MW; 82B93B49E341EC72 CRC64;
 Query Match 67.5%; Score 2042; DB 2; Length 526;
 Best Local Similarity 71.3%; Pred. No. 1.5e-144;
 Matches 373; Conservative 63; Mismatches 71; Indels 16; Gaps 2;
 QY 1 MECLYFLGFLLAARLPDAARFHDVLGNRPSPAYMRHNLGNWSSDENWNEKLYP 60
 Db 1 MESLGGVFLGFLLAAGLPQAARFHDVLGNRPSPAYMRHNLGNWSSDENWNEKLYP 60
 QY 61 VWRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYKNC 120
 Db 61 VWRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYKNC 120
 QY 121 RNEAGLSADPYVNTWTAWSDSGENGTGSHNVFDPGKFFPHHPWRNFIYVHTL 180
 Db 121 RNDLGLTSDLVYVNTWTAGDGDWEDGTSRSHLRFPDRFPFPHGKWSFYVHTL 180
 QY 181 GQYFQKLGRCVRSVNTVNTVLPQPMVTVYRHRGAVPIAQKDVVYVTDQIPV 240
 Db 181 GQYFQKLGRCVRSVNTVNTVLPQPMVTVYRHRGAVPIAQKDVVYVTDQIPV 240
 QY 241 TMFQKDRNSDSEFTFLKDLPIPMFDVLIHDPDVLHDPDGLFVSGDNTGLFVSTNHTVN 300

Db 241 TWSQKDRNLSDEIFLRLDPIVDFVLIHDPDGLFVSGDNTGLFVSTNHTLN 300
 QY 301 HTYVLNGTFTSLNLTAKAAGPCP-----PPPPPPRP-----SKPTPSLGPAGD 344
 Db 301 HTYVLNGTFTSLNLTAKAAGPCP-----PPPPPPRP-----SKPTPSLGPAGD 344
 QY 345 NPLELSRPDENQCNRYGHFOATITIVRGILEVNIQMTDVLMPVPWPESSLIIDFVTC 404
 Db 361 KGMELSDISNENCRINRYGFRTITIVRGILEVNIQMTDVLMPVPWPESSLIIDFVTC 420
 QY 405 QGSIPTVECTIISDPTCEITQNTVSPVDVDMCLLTIVRTFNGSGTVCNLTGLDPTSL 464
 Db 421 KGATPWEACTIISDPTCQIAQNRVCSFPAVDGLCLLSVRAFNFGSGTVCNLTGLDPTSL 480
 QY 465 ALTSTLIISVDPDRDPASPLRMANSLISVCLIAFTVTVISLLVY 507
 Db 481 ALTSTLIISVDPDRDPASPLRMANSLISVCLIAFTVTVISLLVY 523
 RESULT 14
 QNR_COTUA STANDARD; PRT; 559 AA.
 AC 090372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE QNR-71 protein precursor.
 GN Name=QNR-71;
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RC TISSUE=Retina;
 RX MEDLINE=96283633; PubMed=8670835;
 RA Turque N., Demhez F., Martin P., Planque M., Bailly M., Begue A.,
 RA Stehelin D., Saule S.;
 RT "Characterization of a new melanocyte-specific gene (QNR-71) expressed
 in v-myc-transformed quail neuroretina.";
 RL EMBL J. 15:3338-3350 (1996).
 RN [2]
 RP REVISIONS.
 RC TISSUE=Retina;
 RA Saule S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Could be involved in melanogenesis.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Melanocyte-specific, restricted to the
 CC pigmented layer of the retina and the epidermis.
 CC -!- DEVELOPMENTAL STAGE: Transcriptionally regulated by MYC in the
 CC transdifferentiation of embryo pigmented epithelial cells.
 CC Expression precedes melanization.
 CC -!- SIMILARITY: Belongs to the Pmel-17/NMB family.
 CC -!- SIMILARITY: Contains 1 PKD domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X94144; CAA63859.1; -
 DR InterPro; IPR000601; PKD.
 DR Pfam; PF00801; PKD; 1.
 DR PROSITE; PS50093; PKD; 1.
 KW Glycoprotein; signal; Transmembrane.
 FT SIGNAL 1 22 potential.
 CHAIN 23 559 QNR-71 protein.


```
FT DOMAIN 23 487 Extracellular (Potential).
FT TRANSMEM 488 508 Potential.
FT DOMAIN 509 559 Cytoplasmic (Potential).
FT DOMAIN 239 326 PKD.
FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 274 274 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 311 311 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 559 AA; 61713 MW; 81E2793BD6447DD CRC64;

Query Match
Best Local Similarity 53.5%; Pred. No. 1.7e-110;
Matches 297; Conservative 86; Mismatches 157; Indels 15; Gaps 5;

QY 8 LGFILLARLPDAKRFHDVILGNRPSAYMREHNQNGSSDENWNEKLYPVWKRGM 67
Db 8 LALLPAEAVLCAAMRFQDVLNAGR-TAPVTNHRKIQGSSDQKNWNEKLYPFWEEDNP 66
QY 68 RWKNSWKGVRQAVLTSDSPALVGSNITPAVNLIIPRCOKEDANGNIYVKKCRNEAGLS 127
Db 67 RKWDCKGKGVTKLVTSUPLVGSNITPAVNLIIPRCOKEDDGNIIYQRNCTPDSPA 126
QY 128 ADPVYNNATMSDESDGNGTQSHHNVFPDGPFPHPGMRNFIYVFTHTLQGYFOKL 187
Db 127 QDQVYNNTEWIDNCGWENCTSNHSHNVFPDGPFPHPGMRNFIYVFTHTLQGYFOKL 186
QY 188 GRCSVRVSNTANTVILGQLEVTYRRHGRAYVPIAQKQVYVTDQIPVFTVMFQKND 247
Db 187 GRSSANFSVNTANTVILGKHMAVSYRRGHSTYVPIARASTYVYVTDKIPILVSMQKHD 246
QY 248 RNSDDETLKDLPIMFVDVLIHDPSPFLAVSTNYKWSGCDTGLFVSTNHTVHTYVNLG 307
Db 247 RNSDSIFIKSPITFDVKIDHPSYLNDSALSYKWNFGDGLFVSGATTSTFTSLQG 306
QY 308 TFSNLMTVKAAPGCPPPPPPPRPSKPTPSL-----FPAGDNPLELSRIPDNCQI 359
Db 307 NFTNLMTVQAIIPIVPC--KPVTPPTSLPTPAVTTDASSNDSAPSAPNAEDN-PDGGCHI 363
QY 360 NRYGHFQATIIIVGILEVNIQMTDVLMPVWPPESSLIIDFVVTQGSIPTEVCTIISDP 419
Db 364 YRYGYTATITIVGILEVNIQMTSIQMTBSQAEPLVDFVVTQGSFPFTDVCTAVSDP 423
QY 420 TCEITQNTVCSVDVDENCLLTVRRTEGSGTYCVNLTLGDDTSLALTSLISVPRDPA 479
Db 424 TCQVSGQWCVDPVVVTDCEVTIRAFDEPGTYCINITLGDGTSQALASISV---NGG 480
QY 480 SPLRMANSLISVGCALFVTVISLLVYKHKENYPIENSPGNVRSKGLSVFLNRAKAV 539
Db 481 SSSGTTKGVFIPLGLLAVFGLAIGAFVLYKRYKQYPIERSAGQAEQGLSAYVSNFKAF 540
QY 540 FFPNGQEKDPLKQ 554
Db 541 FFPKSTERNPLKSK 555
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RESULT 15

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Q96F58 PRELIMINARY; PRT; 206 AA.
AC Q96F58
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein GPNMB (Glycoprotein (Transmembrane) nmb).
GN Name=GPNMB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
Wilson R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108 (1998).
[5]
RP SEQUENCE FROM N.A.
RA Kalicki J., Kramer J.;
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RA Waterston R.;
Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RA Waterston R.;
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[9]
RP SEQUENCE FROM N.A.
RA Waterston R.;
Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[10]
RP SEQUENCE FROM N.A.
RA Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011595; AAI11595.1; -.
DR EMBL; BT007074; AAP35737.1; -.
DR EMBL; AC005082; AAP22337.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 206 AA; 23945 MW; 30CBDE6928D73FBD CRC64;
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Query Match

Best Local Similarity

Matches 182; Conservative

34.0%;

98.4%;

0;

Score 1029;

Pred. No. 4.2e-69;

0;

DB 2;

Mismatches 3;

Indels 0;

Length 206;

Gaps 0;

QY

1

MECLYFLGFLAARLPDAAKRFHDVLGNERPSAYMREHNQNGWSSDENDWNEKLYP

60

DB

1

MECLYFLGFLAARLPDAAKRFHDVLGNERPSAYMREHNQNGWSSDENDWNEKLYP

60

QY

61

VWKRGMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIYYEKNC

120

DB

61

VWKRGMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIYYEKNC

120

QY

121

RNEAGLSADPYVYNWNTAWSESDGNGTQSHHNVPDGGKPPHHPGWRWNFIYYFHTL

180

DB

121

RNEAGLSADPYVYNWNTAWSESDGNGTQSHHNVPDGGKPPHHPGWRWNFIYYFHTL

180

QY

181

GQYFQ

185

DB

181

GMLLQ

185

Search completed: November 19, 2004, 14:59:05

Job time : 202 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 14:50:11 ; Search time 41 Seconds
(without alignments)
134.180 Million cell updates/sec

Title: US-09-853-880A-17

Perfect score: 3026

Sequence: 1 MECLYFLGLLAARLPD.....PFGNQKDPLLKNQBFKGVG 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3026	100.0	560	2 I38065	gene NMB protein - human
2	659	21.8	626	2 S53871	Pmei 17 protein -
3	622.5	20.6	662	2 I38400	melanoma-associate
4	617.5	20.4	668	2 A41234	melanocyte-specific
5	459	15.2	491	2 A49179	melanoma antigen h
6	136	4.5	926	1 A41105	protein-tyrosine-p
7	120.5	4.0	446	2 T07907	hydroxyproline-tic
8	114.5	3.8	1009	2 C54483	hypothetical prote
9	111.5	3.7	457	2 I55976	hypothetical prote
10	111.5	3.7	555	2 S21766	dihydroliipoamide S
11	109.5	3.6	348	2 A83260	hypothetical membr
12	108	3.6	348	2 T17414	TipC protein - sli
13	106.5	3.5	848	2 T23694	hypothetical prote
14	106	3.5	1874	1 J00533	genome polyprotein
15	105	3.5	492	2 C96521	protein F21D18.18
16	104.5	3.5	363	2 G83306	probable periplasm
17	104.5	3.5	624	1 I51581	transforming prote
18	104.5	3.5	837	2 C69200	surface proteinase
19	104.5	3.5	840	2 B69216	polycystic kidney
20	104.5	3.5	4302	2 A38971	hypothetical prote
21	104	3.4	913	2 T18503	ATP-dependent DNA
22	102.5	3.4	674	2 A10932	retinoblastoma pro
23	102.5	3.4	921	2 A33718	regulatory factor
24	102.5	3.4	979	2 A35913	hypothetical prote
25	101.5	3.4	445	2 D81716	hypothetical prote
26	101	3.3	588	2 T45564	hypothetical prote
27	101	3.3	705	2 T16088	hypothetical prote
28	101	3.3	2014	2 T21560	hypothetical prote
29	100.5	3.3	221	2 T07176	extensin homolog -

ALIGNMENTS

RESULT 1

I38065

gene NMB protein - human

C:Species: Homo sapiens (man)

C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004

C:Accession: I38065

R:Weterman, M.A.; Ajubi, N.; van Dinter, I.M.; Degen, W.G.; van Muijen, G.N.; Ruitter,

Int. J. Cancer 60, 73-81, 1995

A>Title: nmb, a novel gene, is expressed in low-metastatic human melanoma cell lines an

A:Reference number: I38085; MUID:95113576; PMID:7814155

A:Accession: I38065

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-560 <RES>

A:Cross-references: UNIPROT:Q14956; EMBL:X76334; NID:g666042; PIDN:CAA54044.1; PID:g666

C:Genetics:

A:Gene: GDB:NMB

A:Cross-references: GDB:I20237; OMIM:162340

A:Map position: 15q22-15qter

Query Match	Best Local Similarity	Score	DB 2	Length	560;
Matches	560;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Qy	1	MECLYFLGLLAARLPDAAKRFHDLGNERSAYMREHNLQNGWSSDENDWNEKLYP	60		
Db	1	MECLYFLGLLAARLPDAAKRFHDLGNERSAYMREHNLQNGWSSDENDWNEKLYP	60		
Qy	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC	120		
Db	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC	120		
Qy	121	RNEAGLSADPVYVNTAWTAWSEDSDGNGTGSNNVFPDGPFPHPHQRWRFYVHTL	180		
Db	121	RNEAGLSADPVYVNTAWTAWSEDSDGNGTGSNNVFPDGPFPHPHQRWRFYVHTL	180		
Qy	181	GOYFQKLGRCRSVRVSVNTAVTLGPQLMEVTVVRRHGRVYVPIAOVKDVVVTVDIIVFV	240		
Db	181	GOYFQKLGRCRSVRVSVNTAVTLGPQLMEVTVVRRHGRVYVPIAOVKDVVVTVDIIVFV	240		
Qy	241	TMFQKNDNRNSDDETFKDLPIMFVLIHDPSEFLNXTINYKWSFGDNTGLFVSTNHTVN	300		
Db	241	TMFQKNDNRNSDDETFKDLPIMFVLIHDPSEFLNXTINYKWSFGDNTGLFVSTNHTVN	300		
Qy	301	HTVVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSLGPAGDNPLELSRIEDENCQIN	360		
Db	301	HTVVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSLGPAGDNPLELSRIEDENCQIN	360		
Qy	361	RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSILIDFVVTTCQGSIPTEVCTIISDPT	420		
Db	361	RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSILIDFVVTTCQGSIPTEVCTIISDPT	420		

twitching motility
hypothetical prote
lin-1 protein - Ca
hypothetical prote
botulinum neurotox
hypothetical prote
titin, cardiac mus
hypothetical prote
receptor tyrosine
receptor tyrosine
hypothetical prote
platelet-derived g
ATP-dependent DNA
hypothetical prote
hypothetical prote
hypothetical prote

421 CEITQNTVCSVVDVDEMCLLTVRRTFNGSGTVCVNLTLGGDTSLATSLTSLISVPRDPAAS 480
 Db |||||
 421 CEITQNTVCSVVDVDEMCLLTVRRTFNGSGTVCVNLTLGGDTSLATSLTSLISVPRDPAAS 480
 Qy |||||
 481 PLRMANSLISVGCCLAFVTVLSLLVYKHKKEYNPIENSGNVRSKGLSVFLNRAKAVF 540
 Db |||||
 481 PLRMANSLISVGCCLAFVTVLSLLVYKHKKEYNPIENSGNVRSKGLSVFLNRAKAVF 540
 Qy |||||
 541 PFGNQEKDPLLNQKQFKGVS 560
 Db |||||
 541 PFGNQEKDPLLNQKQFKGVS 560
 Qy |||||
 541 PFGNQEKDPLLNQKQFKGVS 560
 Db |||||
 RESULT 2
 Pmel 17 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S53871
 R:Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamaneni, C.; Bennett, D.; Pick
 Nucleic Acids Res. 23, 154-158, 1995
 A:Title: Mouse silver mutation is caused by a single base insertion in the putative cyto
 A:Reference number: S53871; MUID:95175358; PMID:7870580
 A:Accession: S53871
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-626 <KWO>
 A:Cross-references: UNIPROT:Q60696; GB:U14133; NID:g887940; PIDN:AAA69538.1; PID:g887941

Query Match 21.8%; Score 659; DB 2; Length 626;
 Best Local Similarity 27.2%; Pred. No. 3.5e-43;
 Matches 183; Conservative 99; Mismatches 211; Indels 180; Gaps 20;

Qy 7 FLGFLLLAARLPDA--AKRFHDLVGNRPSAYMREHNQNGWSSDENDWNEKLYPVWKR 64
 Db |||||
 9 FLPLVLSALLAVGALSGRNQDLVGRQV-----TKWNRQLYPEWT- 53
 Qy |||||
 65 GDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIVYEKN-CRNE 123
 Db |||||
 54 -EVQGSNCWRGQVSLRVINDGTLVGNASFSIALHFFGSKVLDPDQGVWANNTIING 112
 Qy |||||
 124 AGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDCKPRPHHPGMRNFIYFHTLGOY 183
 Db |||||
 113 SQVWGQPVTP-----QEPDAA-----CVFDDGCPDGPCKPKRSFYVWKTWGKY 159
 Qy |||||
 184 FQKLGRCVRSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDQVYVTDQIPVFVTM 242
 Db |||||
 160 WQVLGGPVSRSSATRAHKLGTHTMEVTVYHRRGSSQYVPLAHASSTFTITDQVPFSVS 219
 Qy |||||
 243 FQKDRNSDETFLKDLPIPMFDVLIHDPSPHFLNYSINYKWSFGDNTGLFVSTNHTVNT 302
 Db |||||
 220 SQLQALDGETKHLRNHPLIFALQLHDPSPGYLAADLSYTWDFDGTGLTISRALDVHT 279
 Qy |||||
 303 YVLNGTFSNLTKVAA-----APGP 322
 Db |||||
 280 YLSSGVSVAQVLOALPLVSCSSPVPGTTDGYMTAEAPTTSRQITTKVGTGTPGQ 339
 Qy |||||
 323 CPPPPP-----PPRPS-----K 334
 Db |||||
 340 MPTTPQSGTTWQMTTEVATTSEQMLTSAVIDTTLAEVSTTEGTGTTTPRPSGTVAQ 399
 Qy |||||
 335 PPSLGPAGNPL-----ELSRPDE-----NCQINRYGHFOATITVE 373
 Db |||||
 400 ATTEGPDAA-SPLLPTQSGTSGISPLDDTDTIMLVKRVPLDCLVLYRGSFSLALDIVQ 458
 Qy |||||
 374 GILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTEVCTIISDPTCEITQNTVCSVD 433
 Db |||||
 459 G-----IESAEILQAVPFSEGDFAELTVSCQGLPKAEACMDISSPCQPPAQLCQSV 512
 Qy |||||
 434 VDEMCLLTVRRTF-NGSGTVCVNLTLGGDTSLATSLTSLISVPRDPAASPLRMANSLISV 492
 Db |||||
 513 PSPDCQLVHLQVLKGGSGTCLNVSADANSLAVASTQLVYPGDGG-----LQAPFLV 567

Qy 493 GCLAFVTVI--SLLV---YKKHKEYN-----PIENSGNVRSKGLSVFLNRAKAVFP 542
 Db |||||
 568 GLLLVIVAVVLAASLTLDLRSRAQPKCHMVVLTAAASGLRARGLG----- 615
 Qy 543 GNOEKDPLLNQKE 555
 Db |||||
 616 ---ENSPILLSGQ 625
 Qy |||||
 616 ---ENSPILLSGQ 625
 Db |||||
 RESULT 3
 I38400
 melanoma-associated ME20 antigen (me20m) - human
 N:Alternate names: melanoma antigen 25
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C:Accession: I38400; A53668; A55753
 R:Marresh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.;
 DNA Cell Biol. 13, 87-95, 1994
 A:Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.
 A:Reference number: I38400; MUID:94235165; PMID:8179825
 A:Accession: I38400
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-662 <RES>
 A:Cross-references: UNIPROT:P40967; EMBL:U01874; NID:g494939; PIDN:AAA18479.1; PID:g494939
 R:Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.
 J. Biol. Chem. 269, 20126-20133, 1994
 A:Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.
 A:Reference number: A53668; MUID:94327568; PMID:7519602
 A:Accession: A53668
 A:Molecule type: mRNA
 A:Residues: 1-592,594-662 <ADB>
 A:Cross-references: GB:S73003; NID:g639589; PIDN:AAC0634.1; PID:g639590
 R:Kawakami, Y.; Elyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.;
 Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994
 A:Title: Identification of a human melanoma antigen recognized by tumor-infiltrating ly
 A:Reference number: A55753; MUID:94294401; PMID:8022805
 A:Accession: A55753
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-161,'F',163-592,594-662 <XAW>
 C:Keywords: glycoprotein

Query Match 20.6%; Score 622.5; DB 2; Length 662;
 Best Local Similarity 25.5%; Pred. No. 2.6e-40;
 Matches 168; Conservative 93; Mismatches 199; Indels 199; Gaps 17;

Qy 3 CLYYFLGFLLLAARLPDAK--RFHDLVGNRPSAYMREHNQNGWSSDENDWNEKLYP 60
 Db |||||
 8 CL---LHLAVIGALLAVGATKVPNRQDLGVSR-----QLR-----TKAWNRQLYP 50
 Qy 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIVYEKN 120
 Db |||||
 51 EMT--BAORLDCWRGQVSLRVINDGTLVGNASFSIALHFFGSKVLDPDQGVWANNT 108
 Qy |||||
 121 RNEAGLSADPYVYN---W---TAWSEDSGNGTQSHHNVFPDCKPRPHHPGMRNFIY 173
 Db |||||
 109 -----INGQVWGQPVYFQETDDA-----CIFDDGCPDGPCKPKRSFYVWK 149
 Qy |||||
 174 IYVFHTLGOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDQVYV 232
 Db |||||
 150 VYVWKWQVQVQLGGPVSGLSIGTGRAMLGTHTMEVTVYHRRGSSQYVPLAHSSAFTI 209
 Qy |||||
 233 TDQIPVFVTMFOKDRNSDETFLKDLPIPMFDVLIHDPSPHFLNYSINYKWSFGDNTGLF 292
 Db |||||
 210 TDQVPFSVSQVLRALDGGNKHFLRNQPLTFALQLHDPSPGYLAADLSYTWDFDGSSTL 269
 Qy |||||
 293 VSTNHTVNTVYVINGTFSNLTKVAAAP-----GPCPPP----- 327
 Db |||||
 270 ISRALVYVTHYLFEPGPVTAQVLOALPLTSCSSPVPGTTDGHRTAEAPNTTAGOVPT 329
 Qy |||||
 328 ----- 327

Db 330 TEVVGTTGQAPTAEPSGTTTQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTL 389
QY 328 -----PPRPSKP----- 335
Db 390 AEMSTPEATGMTPAEVSIVVLGGTTAAQVTTTEWVETARELPPEPEGPDASSIMSTES 449
QY 336 -TPSLGPGAGDNPLELSRIPE---NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVP 391
Db 450 ITGSLGPLDGTATLRLVKRQVPLDCVLYRGSFVTLDIVQ-----IESAEILQAVP 503
QY 392 WPESLIDFVTCQSGIPTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTF-NGSG 450
Db 504 SGEADAFELTVSCQGLPKAEKWEISSPGCQPAQRLCQVLPSPACQLVLHQLKGGSG 563
QY 451 TYCVNLTGLDGTSLATSLTSLISVDRDPASPLRMANSALISVGCCLAFVTVI-SLL 505
Db 564 TYCLNVSLADTNSLAVVSTQLIMP--VPGILLTQGEAGLQGVPLIVGILLVLMVAVLASL 621
QY 506 VYKK 509
Db 622 IYRR 625

RESULT 4
A41234
melanocyte-specific protein Pmel-17 precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 30-Sep-1993
C:Accession: A41234
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.;
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991
A:Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on
A:Reference number: A41234; MUID:92021023; PMID:1924386
A:Accession: A41234
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-668 <KWO>
A:Cross-references: GB:M77348

Query Match 20.4%; Score 617.5; DB 2; Length 668;
Best Local Similarity 25.8%; Pred. No. 6.4e-40;
Matches 171; Conservative 93; Mismatches 197; Indels 203; Gaps 19;

QY 3 CLYFLGFLLLAARLPDAAK--RPHDVLGNRPSPAYMRHNLQNGWSSDENDMNEKLYP 60
Db 8 CL---LHLAVTGALLAVGATKVPKQDNLGYSR-----QLR-----TKAMNRQLYP 50
QY 61 VKRGDMRWKNSKGGVQAVLTSDSPALVGSNITFAVNLIFPRCOKEDANGNIYVEKNC 120
Db 51 EWT--EAQLDCWRGGVSLKVSNDGPTLIGANASFSIALNFPQSKVLPDQGVIVWNT 108
QY 121 RNEAGLSADPVYN---W---TAWSDSDGNGTGQSHHNVFPDQKPFPHHPGWRWNF 173
Db 109 -----IINGSQVWGGQVVPVQETDDA-----CIFPDGQPCSSGSKSHF 149
QY 174 IYVFTLQGVFKLGRCSVRVSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDVVTV 232
Db 150 VYVWKTQYVQVLLGGVPSGLSIGTGRAMLTHMTVEVTVYHRRGSRVYVLAHSSAFTI 209
QY 233 TDQIPVFVTFQKNDNRSSDFTLKDLPIMFDVLHDPHSFLNVTINRYKWSFGDNGCLF 292
Db 210 TDQVPFVSVSQALRDGKNHFLRNQPLTFALQLHDPSCGYLAELSYTWDGDSGSLT 269
QY 293 VSTNHTVNTVLTNGTFSNLTVKAAAP-----GPCPPPP----- 327
Db 270 ISRAPVVTHTYLEPGVTAQVVLQAAIPLTSCGSSVPVGTDDGHRPTAEAPNTAGQVPT 329
QY 328 ----- 327
Db 330 TEVVGTTGQAPTAEPSGTTTQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTL 389
QY 328 -----PPRPSKP----- 335
Db 390 AEMSTPEATGMTPAEVSIVVLGGTTAAQVTTTEWVETARELPPEPEGPDASSIMSTES 449
QY 336 -TPSLGPGAGDNPLELSRIPE---NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVP 391

Db 450 ITGSLGPLDGTATLRLVKRQVPLDCVLYRGSFVTLDIVQ-----IESAEILQAVP 503
QY 392 WPESLIDFVTCQSGIPTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTF-NGSG 450
Db 504 SGEADAFELTVSCQGLPKAEKWEISSPGCQPAQRLCQVLPSPACQLVLHQLKGGSG 563
QY 451 TYCVNLTGLDGTSLATSLTSLISVDRDPASPLRMANSALISVGCCLAFVTVI-SLL 505
Db 564 TYCLNVSLADTNSLAVVSTQLIMP--VPGILLTQGEAGLQGVPLIVGILLVLMVAVLASL 621
QY 506 VYKK 509
Db 622 IYRR 625

RESULT 5
A49179
melanoma antigen homolog rpe1 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49179; I45861
R:Kim, R.Y.; Wistow, G.J.
Exp. Eye Res. 55, 657-662, 1992
A:Title: The cDNA RPE1 and monoclonal antibody HMB-50 define gene products preferential
A:Reference number: A49179; MUID:93122163; PMID:1478275
A:Accession: A49179
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-491 <KIM>
A:Cross-references: UNIPROT:Q06154
A:Experimental source: retinal pigment epithelium
A:Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBI:122439)
C:Genetics:
A:Gene: RPE1

Query Match 15.2%; Score 459; DB 2; Length 491;
Best Local Similarity 26.6%; Pred. No. 8.7e-28;
Matches 122; Conservative 64; Mismatches 130; Indels 142; Gaps 12;

QY 182 QYFKLGRCSVRVSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDVVTVTDQIPV 240
Db 1 QYQVVLGGVPSGLSIGTDKAMLTGYNMEVTVYHRRGSSQSYVPLAHSSAFTITDQVPFSV 60
QY 241 TMFQKNDNRSSDFTLKDLPIMFDVLHDPHSFLNVTINRYKWSFGDNGTGLFVSTNHTVN 300
Db 61 SVSOLQALDGRNKRFLRKQPLTFALQLHDPSCGYLAGADLSYTWDFDGTGLISRALVT 120
QY 301 HTYVLTNGTFSNLTVKAAAP---GPCPPPPPPPP----- 331
Db 121 HTYLESGPVTAQVVLQAAIPLTSCGSGFVPGTDDRHVTAEAPGTAGQVPTTEVMGTT 180
QY 332 ----- 333
Db 181 GOVPTAEAPGTTVGVVPTTEDVGTTPQVATSKVLSTTPVEMPTAKATGRTPVSTTEPS 240
QY 334 KPTPSLG-----PAGDN-----PLE-----LSRIPE----- 355
Db 241 GTTVTQGTTPBELVETTAGEVSTPEPAGSNTSSFPTEGTAGSLSPLEDDTATLVLEKQA 300
QY 356 --NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVTCQSGIPTEVC 413
Db 301 PLDCVLYRGSFVTLDIVS-----IESAEILQAVSSGESGDAFELTVSCQGLPKAE 353
QY 414 TIISDPTCEITQNTVCSVDVDEMCLLTVRRTF-NGSGTYCVNLTGLDGTSLATSLTSLIS 472
Db 354 MDLSSPCQPLPAQRLCQVPPSPACQLVLHQLKGGSGTYCLNVSLADNSLAVVSTOLV 413
QY 473 VPRDRDPASPLRMANSALISVGCCLAFVTVI-SLLVYKK 509
Db 414 MPQGE--AGLRQAP---LFGVILLVLTALLASLIYRR 446

RESULT 6

A;Cross-references: UNIPROT:O22456; EMBL:AF015883; NID:G2384727; PIDN:AAB69862.1; PID:1
A;Experimental source: gametes
C:Genetics:
A:Gene: GAS28
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-446/Product: hydroxyproline-rich glycoprotein GAS28 #status predicted <MAT>

Query Match 4.0%; Score 120.5; DB 2; Length 446;
Best Local Similarity 29.5%; Pred. No. 0.16;
Matches 38; Conservative 7; Mismatches 38; Indels 46; Gaps 6;

QY 320 PGCPPPPPPPPRSKTPSLGPA-----GDNPLELSRIPDENCOINRYGHQF 366
DB 240 PPSPPPPPPPTSPSPPELPPAQDPAPARKRPPPPASPPPPRDFPFCQCORNARGSL 299
QY 367 AT-----ITIVEGILEVNI-IQMTDVLMPVPWPESSLIDFVVTQGS IPTVC----- 413
DB 300 MTASNNITVVGNGTRICFNVALKD-----CEN--PNSKCCFEFELYK 340
QY 414 -TIISDPTC 421
DB 341 MEIEADPTC 349

RESULT 8
C64483
hypothetical protein MJ1468 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: C64483
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64483
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1009 <BUL>
A;Cross-references: UNIPROT:Q58863; GB:U67587; GB:L77117; NID:G1592103; PID:G1592109;
C;Genetics:
A;Map position: FOR1437031-1440060

Query Match 3.8%; Score 114.5; DB 2; Length 1009;
Best Local Similarity 18.3%; Pred. No. 1.4;
Matches 88; Conservative 58; Mismatches 157; Indels 177; Gaps 19;

QY 100 LIPFCCKEDANGNIVVEKNCNEAGL-----SADPPVY----- 133
DB 490 LYYPHFVVDNGNI-----EVGIPPIGVGGYSSVPQIYASPTIAPTVPYINITIV 541
QY 134 ---NWT-AWSEDSGCGNTGSHNVFPDGKFPFPHPGWRNWFYVFTLGOYFOKLGR 189
DB 542 EPASWTYVW-----HHIYFGDGSWIKPKKSPYTFTHYTSSEGVY----- 582
QY 190 CSVRVSNTANVTILGPQLMEVTVYRRHGRAYVPIAQKDVVVYVDQIPVFVTMFQKNDRN 249
DB 583 -PIYMKVYTA-----NMKTVYVDNKNPIAKLYINPNAS 617
QY 250 SSDE-----TFLKDLPI-----FDVLHDPDSHELN 275
DB 618 YKDTISPSINSDPANRMIPYNYGTIGYIPSPNSPMARYIGFNLTVYD----- 671
QY 276 YSTINYKWSFGDNTGLFVSTNHTV-NHT---YVLNGTSLNLTVKAAAGPCPP----- 326
DB 672 -SNGVAMNYSNELTIISKFPICNYTAKLVVDMGCVNSTTVKFSVINRPPVAQFIY 730
QY 327 -PPPRPSKP-----TPSLGPAGDNPLELSRI PDENC-----QINRYGHFOATITI 371
DB 731 VQVSTFATNRYVEVSGVSDRCEIAVVTWNKCGCTVINTDTITVHHKHSRPGVYVTLTV 790

Query Match 3.6%; Score 109.5; DB 2; Length 348;
 Best Local Similarity 21.2%; Pred. No. 0.8;
 Matches 83; Conservative 51; Mismatches 128; Indels 129; Gaps 22;

QY 61 VVKRGDMKWSKG--GRVOAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVVEK 118
 DB 16 VFETQTKLSATTGNDGTATILRN--AAGGGIVTVCVL-----DADGKV--SD 63
 QY 119 NCR-NEAGLSADPYVYNWTAMSEDSGNGTQSHNVPFDPKPPHFGHWRWFIYF 177
 DB 64 QCDVHFAAVSAD--IISFSVSATDPLGYSNNGKA-ARVFAELIPSPNPN--VTNCLINF 117
 QY 178 HTLG-----QYFQKLGCSVRVSVNTANVTLPOLMEVTVYRRHGRAVPIAQKDVV 231
 DB 118 STFGVSGIINNYVNIIGEPN-----SVSGPSLMQ-----FVQIGNTKT-- 157
 QY 232 VTDQIPVFTVMFQKDRNSDDETFKDLPIPMEDVLHDPHSFLNYSNTINYSFGDNTGL 291
 DB 158 ----IPV-----DVSXKGE-----EGSVGIGQAL 178
 QY 292 FVSTNHTVNHVYVLTGFTSL---NLTVKAAAGCPGPPPPPPRPSKPTSLGPDAGNPLE 348
 DB 179 VTTQTP-----DKAFALSTPNARVDINPAP-PPPPPPSPCPPPPPPPPPPPVR 229
 QY 349 LS-----RIPDENCQINRGHFQATITIVEGILEVNIQMTDVLMPVMPWESS 396
 DB 230 PSYTIQIDAVDNIPIPTGRGIARVTVFQNGRPLAGALVQCSLSLSG-----NTS 281
 QY 397 LIDFVTCQSGSIPTVCTIISDPTCEITQNT 427
 DB 282 LM-FALAA-----NEIANLVSP-----QNT 301

RESULT 12

T17414
 TipC protein - slime mold (Dictyostelium discoideum)
 C:Species: Dictyostelium discoideum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R:Accession: T17414
 R:Stages: J.T.; Laub, M.T.; Loomis, W.F.
 submitted to the EMBL Data Library, July 1998
 A:Description: Interaction of tip genes in early Dictyostelium discoideum development.
 A:Reference number: Z18774
 A:Accession: T17414
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3848 <STE>
 A:Cross-references: UNIPROT:O76737; EMBL:AF079445; NID:G3420744; PID:G3420745; PIDN:AA03
 A:Experimental source: strain AX4
 C:Genetics:
 A:Gene: tipC
 A:Introns: 72/3
 A:Function:
 A:Description: required for tip formation

Query Match 3.6%; Score 108; DB 2; Length 3848;
 Best Local Similarity 19.0%; Pred. No. 28;
 Matches 69; Conservative 55; Mismatches 132; Indels 108; Gaps 14;

QY 3 CLYVFLGLLAARLPDAAKRFHDVLGNERPSAYMRHNQNGWSSDENDWNEKLYPVW 62
 DB 918 QYVNLVNIISQVTPIDQOQO---LIGSE--SWMSAFDYSVYQSNIFKQPQOLQPOQ 972
 QY 63 KRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVVEKCRN 122
 DB 973 KQ-----QSPPLISSP-----PLIKKKKSYSKFEIDSXKMF 1003
 QY 123 EAGLSADPY-----VYNWTAWSEDSGNGTQSH-----HNVPDGRKPPHHPGWR 170
 DB 1004 EASPNIDKFNHLRLDNYDSGSSNNDSSNTTNNHQLVSHV-----1048
 QY 171 WNFYVFTHTLQYFQKLGRCVRSVSN---TANVTLPQMLMEVTVYRRHGRAVPIAQVK 227

Db 1049 -ALVYLRCLHGTYYVQKLFDTNLELLIKGMWIEDCFQKQPSI-----AHGSG----- 1093
 QY 228 DVYVVTQIPVFTVMFQKDRN-----SDETFKDLPIPMFVLIHDP 270
 DB 1094 -----GDYLAATTTRFRKENDVNIIGGSGNENLIKFKIQIISDSPPYNNIDKLLDIELSQI 1148
 QY 271 SHFLNYSNTINYSFGDNG--TGLFVSTNHTVNHVYVLTGFTSLNLTVKAAPG---PCPPP 326
 DB 1149 NLLNRKIVAGLIEFSNSVLSILKNQNNQ---NNNQNNQNNINSSPTVFTSPPP 1205
 QY 327 PPPP 330
 DB 1206 PPPP 1209

RESULT 13

T23694
 hypothetical protein M03C11.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R:Accession: T23694
 R:McMurray, A.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: Z19783
 A:Accession: T23694
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-848 <WIL>
 A:Cross-references: UNIPROT:Q21489; EMBL:Z49128; PIDN:CAA88959.1; GSPDB:GN00021; CESP:N
 A:Experimental source: clone M03C11
 C:Genetics:
 A:Gene: CESP:M03C11.2
 A:Map position: 3
 A:Introns: 113/2; 147/3; 185/3; 379/1; 482/3; 553/2; 688/3; 762/3

Query Match 3.5%; Score 106.5; DB 2; Length 848;
 Best Local Similarity 20.8%; Pred. No. 4.6;
 Matches 117; Conservative 75; Mismatches 203; Indels 167; Gaps 30;

QY 83 TSDSPALV--GSNITFAVN-----LIPRCOKEDANGNIVVEKCRNEAGLSADP 130
 DB 206 TRQPRIVTCASRGTLUCVNEEVKLLKLNHLNKEKMLKNGKSEKVKQLEKGTTKT 265
 QY 131 YV-----YNWTAWSEDSG-----ENGTOGSHNVFPDGKPF----- 162
 DB 266 KTCATSCFEYNSTQIEDVWVGLSNKLTSLVSKQGLSNGCPYFATRKSVFPQCOLVLL 325
 QY 163 PH-----HPCWRR-W-----NFYI-----VFHTLQYF-----OKLGR-----CSV-RVS 195
 DB 326 PYQVLLHDGTRKAWGIELKDNVIVLDEAHNVLTISFFFRKLEKSVKNGFKNCSLYSAE 385
 QY 196 VNTANVTLPQMLMEVTVYRRHGRAYV---PIAQKDVVVTQIPVFTVMFQKDRNSSD 252
 DB 386 ISTKSUTLALRL--IREYNHAYKLLAHNLLYMKQLESLSKMLIFLNSQSKEDVMTMA 443
 QY 253 ETEFKDLPIPMFVLIHDPHSFLNYSNTINYSFGDNGTGLFVSTN---HTVNHVYVLTG 308
 DB 444 Q-LARNLNL-EINLFKLAEMYMEKTDLCCKFH-----GFYMRLOKBEIKKENEKPKLTGI 496
 QY 309 FSNLTVKAAAGCPGPPPPPPPPRPSKPTP-----SLGPAGDNPLELSRIIDENCQINRYG 363
 DB 497 QKL-MAAKEAPEPEAPLPPPKP-VESPLFSLKSFIDALTNKCEDGRIIVEKSAEAKF 554
 QY 364 HF-----QATITIVEGILEVNIQMTDVLMPVMPWESSLIDFVFTVCOGS 407
 DB 555 RFMLNLPADRLSEVVTISARATI-LVGTM-----PAQLLVE--TLSEGS 596
 QY 408 IPTEVCTIISDPTCEITQNTVCSVDVDEMCILTIVRTFNGSGTYCNLTGLDGTSLALT 467
 DB 597 IGAD-----SIRRFSCCHVIDDSQLLAIVTERTVDGKPFQLTQYTRGADTTLSRL 646
 QY 468 STLISVDPDRDPASPLRMANGSLIS--VGCLAIFTVVISLL--VYKKEKYNPIENSPGNV 523

protein F1D18.18 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C96521
R/Theologians, A.; Ecker, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 916-920, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:50:36 ; Search time 39 Seconds
(without alignments)
952.258 Million cell updates/sec

Title: US-09-853-880A-17
Perfect score: 3026
Sequence: 1 MECLYFLGLLLAARPLD.....FPCNQEKDPLLKNQEFKGVY 560

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3026	100.0	560	1 US-09-985-799-90	Sequence 90, Appl
2	3026	100.0	560	1 US-09-977-371-90	Sequence 90, Appl
3	3026	100.0	560	1 US-08-594-031-90	Sequence 90, Appl
4	3026	100.0	560	4 US-09-643-597-225	Sequence 225, App
5	3026	100.0	560	4 US-09-480-884A-225	Sequence 225, App
6	3026	100.0	560	4 US-09-542-615A-225	Sequence 225, App
7	3026	100.0	560	4 US-09-606-421B-225	Sequence 225, App
8	3026	100.0	560	4 US-09-476-496A-225	Sequence 225, App
9	3026	100.0	560	4 US-09-630-940B-225	Sequence 225, App
10	2197	72.6	574	3 US-09-383-586-36	Sequence 36, Appl
11	2197	72.6	574	4 US-09-823-038A-36	Sequence 36, Appl
12	2179	72.0	572	4 US-09-197-970B-5	Sequence 5, Appl
13	969	32.0	376	1 US-09-985-799-100	Sequence 100, App
14	969	32.0	376	1 US-09-985-799-102	Sequence 102, App
15	969	32.0	376	1 US-09-977-371-100	Sequence 100, App
16	969	32.0	376	1 US-09-977-371-102	Sequence 102, App
17	969	32.0	376	1 US-08-594-031-100	Sequence 100, App
18	969	32.0	376	1 US-08-594-031-102	Sequence 102, App
19	622	20.6	661	2 US-08-417-174-121	Sequence 121, App
20	622	20.6	661	3 US-09-267-439-121	Sequence 121, App
21	622	20.6	661	4 US-08-388-852B-2	Sequence 2, Appl
22	622	20.6	661	4 US-09-073-138-121	Sequence 121, App
23	621	20.5	661	2 US-08-417-174-27	Sequence 27, Appl
24	621	20.5	661	2 US-08-231-565A-27	Sequence 27, Appl
25	621	20.5	661	2 US-09-007-961-27	Sequence 27, Appl
26	621	20.5	661	3 US-09-267-439-27	Sequence 27, Appl
27	621	20.5	661	4 US-09-073-138-27	Sequence 27, Appl

28 603.5 19.9 668 1 US-07-891-942G-6 Sequence 6, Appl
29 238.5 7.9 190 4 US-08-388-852B-35 Sequence 35, Appl
30 236 7.8 202 4 US-08-388-852B-38 Sequence 38, Appl
31 233.5 7.7 192 4 US-08-388-852B-37 Sequence 37, Appl
32 233 7.7 197 4 US-08-388-852B-36 Sequence 36, Appl
33 136.5 4.5 71 1 US-09-985-799-98 Sequence 98, Appl
34 136.5 4.5 71 1 US-09-977-371-98 Sequence 98, Appl
35 136.5 4.5 71 1 US-08-594-031-98 Sequence 98, Appl
36 116 3.8 742 4 US-09-489-039A-7998 Sequence 98, Appl
37 112 3.7 440 4 US-09-248-796A-26860 Sequence 26860, A
38 111 3.7 429 4 US-09-252-991A-31611 Sequence 31611, A
39 108 3.6 1158 4 US-09-313-942-26 Sequence 26, Appl
40 108 3.6 4302 3 US-08-658-136-5 Sequence 5, Appl
41 107.5 3.6 4302 3 US-08-658-136-5 Sequence 5, Appl
42 106 3.5 859 4 US-09-313-942-7 Sequence 7, Appl
43 105.5 3.5 427 3 US-08-705-771-16 Sequence 16, Appl
44 105.5 3.5 427 4 US-09-417-540-16 Sequence 16, Appl
45 105.5 3.5 4303 2 US-08-460-751-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-985-799-90
; Sequence 90, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/985,799
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:

US-09-985-799-90

APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remerick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: OA16-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>

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/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 560 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-977-371-90

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RESULT 3
US-08-594-031-90
; Sequence 90, Application US/08594031
; Patent No. 5783182

Query Match	100.0%;	Score 3026;	DB 1;	Length 560;
Best Local Similarity	100.0%;	Pred. No. 4.9e-269;		
Matches 560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	MECLLYFGLFLLAARLPDAAKRFHDVLGNERPSAYMREHNQNLNGSSDENDWNEKLYP	60		
1	MECLLYFGLFLLAARLPDAAKRFHDVLGNERPSAYMREHNQNLNGSSDENDWNEKLYP	60		
61	VNKRGDWRKNSWKGRYQVAULTSDPALVGSNITFAVNLIPPRCKEDANGNIVYEKNC	120		
61	VNKRGDWRKNSWKGRYQVAULTSDPALVGSNITFAVNLIPPRCKEDANGNIVYEKNC	120		
121	RNEAGLSADPYYYNWTAMSEDSGNGTQGSHHNVFDPGKPPHHPGWRWNFIYVFEHTL	180		
121	RNEAGLSADPYYYNWTAMSEDSGNGTQGSHHNVFDPGKPPHHPGWRWNFIYVFEHTL	180		
181	GOYFQKLGRCSSVRVSVNTANVTLPQLMEVTVYRRHGAYVPIAQVKDVIYVVTQDIPFV	240		
181	GOYFQKLGRCSSVRVSVNTANVTLPQLMEVTVYRRHGAYVPIAQVKDVIYVVTQDIPFV	240		
241	TFMQKNDNRNSDETFELKOLPIMFVDVLIDHPSHFLNYSTINWKSEGDNTGLFVSTNHTVN	300		
241	TFMQKNDNRNSDETFELKOLPIMFVDVLIDHPSHFLNYSTINWKSEGDNTGLFVSTNHTVN	300		
301	HTVVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGAGDNPLELSRIPDENCOIN	360		
301	HTVVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGAGDNPLELSRIPDENCOIN	360		
361	RYGHFOATITIVEGILEVNNIIQMTDVLMPVPWPRESSLIDFVVVTCOGSIPTVECVTIISDPT	420		
361	RYGHFOATITIVEGILEVNNIIQMTDVLMPVPWPRESSLIDFVVVTCOGSIPTVECVTIISDPT	420		
421	CEITQNTVCSVDVDEMCLLTIVRRTFENGSGTVCVNLTLTGDDTSALTSTLISVDPDPAS	480		
421	CEITQNTVCSVDVDEMCLLTIVRRTFENGSGTVCVNLTLTGDDTSALTSTLISVDPDPAS	480		
481	PLRMANSALISVGCLAI FVTVISLLVYKHKKEYNPENSPGNVNRSKGLSYFLNRAKAVF	540		
481	PLRMANSALISVGCLAI FVTVISLLVYKHKKEYNPENSPGNVNRSKGLSYFLNRAKAVF	540		
541	FPGNQEKDPLLNQNEFKGVS	560		
541	FPGNQEKDPLLNQNEFKGVS	560		

RESULT 2
US-09-977-371-90
; Sequence 90, Application US/09977371
; Patent No. RE38490
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,371
; FILING DATE: 16-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996

Db	361	RYGHEQATITIV	EGLEVNIIQMTDVLMPVP	PSSSLIDFVVT	CQSIPTEVCTII	SDPT	420
Qy	421	CEITQNTVCS	PVDVDEMCLLT	VRRTFNGSGTY	CVNLTGLGDDT	SLALTSLTSLISV	PD
Db	421	CEITQNTVCS	PVDVDEMCLLT	VRRTFNGSGTY	CVNLTGLGDDT	SLALTSLTSLISV	PD
Qy	481	PLRWANSALIS	VGCLAI	FVTVISLLVYK	HKHKNPIENS	PGNVRSKGLSV	FLNRAKAVF
Db	481	PLRWANSALIS	VGCLAI	FVTVISLLVYK	HKHKNPIENS	PGNVRSKGLSV	FLNRAKAVF
Qy	541	FPGNOEKD	PLLKNQ	BEFGVS	560		
Db	541	FPGNOEKD	PLLKNQ	BEFGVS	560		
<div> <div>RESULT 4</div> <div> US-09-643-597-225 ; Sequence 225, Application US/09643597 ; Patent No. 6426072 ; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong ; APPLICANT: Fan, Liqun ; APPLICANT: Kalos, Michael D. ; APPLICANT: Bangur, Chaitanya S. ; APPLICANT: Hosken, Nancy ; APPLICANT: Fanger, Gary R. ; APPLICANT: Li, Samuel X. ; APPLICANT: Wang, Aijun ; APPLICANT: Skeiky, Yasir A.W. ; APPLICANT: Henderson, Robert A. ; APPLICANT: McNeill, Patricia D. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.455C11 ; CURRENT APPLICATION NUMBER: US/09/643,597 ; CURRENT FILING DATE: 2000-08-21 ; NUMBER OF SEQ ID NOS: 369 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO 225 ; LENGTH: 560 ; TYPE: PRT ; ORGANISM: Homo sapien US-09-643-597-225 </div> </div>							
<div> <div>Query Match</div> <div> Best Local Similarity 100.0%; Score 3026; DB 4; Length 560; Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0 </div> </div>							
Qy	1	MECLYYFLG	FLLLAARLP	LDAAARFHDV	LGNRP	SAVMREHNLQ	NGSSDENDWNEKLYP
Db	1	MECLYYFLG	FLLLAARLP	LDAAARFHDV	LGNRP	SAVMREHNLQ	NGSSDENDWNEKLYP
Qy	61	VMKRGDMRW	KNWSKMG	GRVQAVLT	SDSPALVGS	NTTAVNLI	FERCOKEDANGNI
Db	61	VMKRGDMRW	KNWSKMG	GRVQAVLT	SDSPALVGS	NTTAVNLI	FERCOKEDANGNI
Qy	121	RNEAGLSAD	PYYVNW	TAWSDSDG	ENGTCGSH	HNVPD	KGKFP
Db	121	RNEAGLSAD	PYYVNW	TAWSDSDG	ENGTCGSH	HNVPD	KGKFP
Qy	181	GQYFQK	LGRC	SVRVSV	VNTANVT	LGPOLME	VTVYRRHGR
Db	181	GQYFQK	LGRC	SVRVSV	VNTANVT	LGPOLME	VTVYRRHGR
Qy	241	TMFQKNDR	NSSDET	FLKDL	PI	MFDDVLI	HPSPHFLN
Db	241	TMFQKNDR	NSSDET	FLKDL	PI	MFDDVLI	HPSPHFLN
Qy	301	HTYVLNGT	FSLNL	TVKAA	APGCP	PPPPPP	PPPSKPT
Db	301	HTYVLNGT	FSLNL	TVKAA	APGCP	PPPPPP	PPPSKPT

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QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
QY 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
Db 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
QY 541 PFGNOEKDPLLKNQBFKGV 560
Db 541 PFGNOEKDPLLKNQBFKGV 560
QY 541 PFGNOEKDPLLKNQBFKGV 560
Db 541 PFGNOEKDPLLKNQBFKGV 560
RESULT 6
US-09-542-615A-225
; Sequence 225, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-542-615A-225
Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMRHNLGWSNDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMRHNLGWSNDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTCGSHNVFPDGPFPHPGWRWNFIYVPHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTCGSHNVFPDGPFPHPGWRWNFIYVPHTL 180
QY 181 GOYFQKLGRCSVRVSNTANTVTLGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDQIPFV 240
Db 181 GOYFQKLGRCSVRVSNTANTVTLGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDQIPFV 240
QY 241 TMEQKNDNRSSDDETFKDLPIMFVLIHDPHSHFLNYSTINYNKWSFGDNTGLFVSTNHTN 300
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QY 301 HTYVLNGTFSNLNITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPENCQIN 360
Db 301 HTYVLNGTFSNLNITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPENCQIN 360
QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
QY 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
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QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
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Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
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Db 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
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Db 541 PFGNOEKDPLLKNQBFKGV 560
RESULT 5
US-09-480-884A-225
; Sequence 225, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-480-884A-225
Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMRHNLGWSNDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120
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QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTCGSHNVFPDGPFPHPGWRWNFIYVPHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTCGSHNVFPDGPFPHPGWRWNFIYVPHTL 180
QY 181 GOYFQKLGRCSVRVSNTANTVTLGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDQIPFV 240
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QY 301 HTYVLNGTFSNLNITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPENCQIN 360
Db 301 HTYVLNGTFSNLNITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPENCQIN 360
QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVPWPESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLALTSTLISVDPDRPAS 480
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Db 481 PLRMANALISVGCIAIFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLKNQEFKGV 560
Db 541 FPGNQEKDPLLKNQEFKGV 560

RESULT 7

US-09-606-421B-225
; Sequence 225, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liyun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-225

Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
QY 61 VMKGRDMRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKQEDANGNIYVEKNC 120
Db 61 VMKGRDMRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKQEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRWNFIYVPHL 180
Db 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRWNFIYVPHL 180
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Db 181 GOYFQKLGRCVRSVSVNTANVTILGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240
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QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLLIDFVVTCCGSIPTVEVCTIISDPT 420
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Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTGLDDTSALSTLISVDRDPAS 480
QY 481 PLRMANALISVGCIAIFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540
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Db 481 PLRMANALISVGCIAIFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540
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Db 541 FPGNQEKDPLLKNQEFKGV 560

RESULT 8

US-09-476-496A-225
; Sequence 225, Application US/09476496A
; Patent No. 6706262
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476,496A
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-476-496A-225

Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60
QY 61 VMKGRDMRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKQEDANGNIYVEKNC 120
Db 61 VMKGRDMRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKQEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRWNFIYVPHL 180
Db 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGWRWNFIYVPHL 180
QY 181 GOYFQKLGRCVRSVSVNTANVTILGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240
Db 181 GOYFQKLGRCVRSVSVNTANVTILGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240
QY 241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPSSHFLNYSTINVKWFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPSSHFLNYSTINVKWFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVWPWPESSLLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTGLDDTSALSTLISVDRDPAS 480
Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTGLDDTSALSTLISVDRDPAS 480
QY 481 PLRMANALISVGCIAIFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANALISVGCIAIFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLKNQEFKGV 560
Db 541 FPGNQEKDPLLKNQEFKGV 560

RESULT 9

```

US-09-630-940B-225
; Sequence 225, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND
; TITLE OF INVENTION: AND DIAGNOSIS OF
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: Fast-Seq for Windows Version
; SEQ ID NO 225
; LENGTH: 560
; TYPE: Prt
; ORGANISM: Homo sapien
US-09-630-940B-225

```

	Query Match	100.0%;	Score 3026;	DB 4;	Length 560;
	Best Local Similarity	100.0%;	Prod. No. 4,9e-269;		
	Matches 560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MECLYYFLGFLLLAARLP	LDAAKRPHDVLGNERPSAYMR	EHNLQNGSSDENDWNEKLYP	60
Db	1	MECLYYFLGFLLLAARLP	LDAAKRPHDVLGNERPSAYMR	EHNLQNGSSDENDWNEKLYP	60
Qy	61	VWKGDMRWKNSWKGGRVQAVL	TSDSPALVGSNITFAVNLI	FPKCKEDANGNTIYVKNC	120
Db	61	VWKGDMRWKNSWKGGRVQAVL	TSDSPALVGSNITFAVNLI	FPKCKEDANGNTIYVKNC	120
Qy	121	RNEAGLSADPVYYNWTAWSEDS	CGENGTCQSHHNVPD	GGKFPHPHGWRRWNFIYVFHTL	180
Db	121	RNEAGLSADPVYYNWTAWSEDS	CGENGTCQSHHNVPD	GGKFPHPHGWRRWNFIYVFHTL	180
Qy	181	GOYFQKLGRCSVRSVNTANVT	LGPQLMEVTVYRRHGRAYVPI	IAQVKDVVYVTDQIPVFV	240
Db	181	GOYFQKLGRCSVRSVNTANVT	LGPQLMEVTVYRRHGRAYVPI	IAQVKDVVYVTDQIPVFV	240
Qy	241	TMFOKNDNRNSSDETFLKDL	PIMFDVL IHDPSHF	LNYSNTINKWFGDNTGLFVSTNHTVN	300
Db	241	TMFOKNDNRNSSDETFLKDL	PIMFDVL IHDPSHF	LNYSNTINKWFGDNTGLFVSTNHTVN	300
Qy	301	HTVYLNGTFSNLTVKAAAPG	CPPPPPPPSPKPTPSL	GPAGDNPLELSRIPDENCQIN	360
Db	301	HTVYLNGTFSNLTVKAAAPG	CPPPPPPPSPKPTPSL	GPAGDNPLELSRIPDENCQIN	360
Qy	361	RYGHFQATITIVEGILEYNI	IIQMTDVLMPVPWP	SSSLIDFVVTCQGSIPTEVCTIISDPT	420
Db	361	RYGHFQATITIVEGILEYNI	IIQMTDVLMPVPWP	SSSLIDFVVTCQGSIPTEVCTIISDPT	420
Qy	421	CEITQNTVCS PVDVDEMCLL	TVRRTPFNGSGTYCVNLT	GLGDDTSALTSTLLSVDPDRDPAS	480
Db	421	CEITQNTVCS PVDVDEMCLL	TVRRTPFNGSGTYCVNLT	GLGDDTSALTSTLLSVDPDRDPAS	480
Qy	481	PLRMANSALISVGCIAIF	VTVISLLVYKKHKEYNP	IENTSPGNVRSKGLSVFLNRAKAVF	540
Db	481	PLRMANSALISVGCIAIF	VTVISLLVYKKHKEYNP	IENTSPGNVRSKGLSVFLNRAKAVF	540
Qy	541	FPGNQEKDPLLNQNEFKGVS	560		
Db	541	FPGNQEKDPLLNQNEFKGVS	560		

RESULT 10

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US-09-383-586-36
; Sequence 36, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin
; APPLICANT: Onrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Mouse
; US-09-383-586-36

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Query Match	72.6%	Score 2197	DB 3	Length 574
Best Local Similarity	70.7%	Pred. No. 6.3e-193		
Matches	403	Conservative	69	Mismatches 82
			Indels	16
			Gaps	2
Qy	1	MECLYIFLGFLLLAARLPDAARFHDVLGNRPSPAYMRBHNOLNGWSSDENDWNEKLYP	60	
Db	1	MESJCGVLGFLLLAAGLPQAAKFRDVLGHEQYPNHRHNQLRGWSSDENEDWDEHLYP	60	
Qy	61	VWKEGDMRWKNSMKGRVQAVLTSDSPALVGSNIITFAVNLIFPRCKEDANGNIIVYEKNC	120	
Db	61	VWREGDGRKXDSWEGGRVQAVLTSDSPALVGSNIITFVNLVFPRCQEDANGNIIVYEKNC	120	
Qy	121	RNEAGLSADPYVYVNTWATWSEDSGENTGQSHNVFPDGKFPFPHHPCWRBWNFIYVVFHTL	180	
Db	121	RNDJGLTSDLVHVNMTAGADGDWEDGTSRQHLRFPDRRFPPHPCWKKMSFVYVVFHTL	180	
Qy	181	GOYFQKLGRCSVRSVNTANVTLPQLMWVTVVRRHGRAYVPIAQKDVVVVTDQIIPFV	240	
Db	181	GOYFQKLGRCARSIVTNLTAGPQWVEVTVFRYGRAYIPISKVDVVVTDQIIPFV	240	
Qy	241	TMFQKDRNSSDETFLKDLPIMFEDVLIHDPESHFNLYSTINYYKSGFGNTGLFVSTNHTVN	300	
Db	241	TMSQKDRNLSDIEFLRDLPIVFQVLIHDPESHFNLSAISYKMNFGDNTGLFVSNHNTLN	300	
Qy	301	HTYVYNGTFSNLITVKAAAPGCP-----PPPPPPR-----SKPTPSLGPAGD	344	
Db	301	HTYVYNGTFNLNLITVQATVAPGCPSPSPSTPPSPSPSPPLTSLTSPSPSLMTGY	360	
Qy	345	NPLELSRPDENCOINRYXGHFOAIIITVEGILEYNIITQMTDVLMPVMPBSSLIDFVVTC	404	
Db	361	KSMELSDISNENCRINRYGYPRATITVEGILEVSIINQIADVMPPTQPANSLMDFVTC	420	
Qy	405	QGSITPEVCTIISDPTCEITONTVCSPVDVDEMCLLTVRRTRFNGSGTYCVNLITLGDTSL	464	
Db	421	KGATPEMACTIISDPTCQIAQNRVCSPVANDGCLLSVRRAFNGSGTYCVNFTLGDGASL	480	
Qy	465	ALTSTLIISVPDRDASPLRMANSALISVGCLAIFFVTISLLVYKKHKEYNPENSGNVV	524	
Db	481	ALTSTLIISPGKDPDSPRAVNGVLIISGCLAVLVTWVITLLYKKHKEYIGNCPRTV	540	
Qy	525	RSKGLSVFLNRAKAVFFPGNGEKDPLLNQ	554	
Db	541	KKGKISVLLSHAKAPFFRGDQKQDPLLODK	570	

RESULT 11
US-09-823-038A-36

; Sequence 36, Application US/09823038A

; Patent No. 6797271

; GENERAL INFORMATION:

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Abernethy, Nevin

; APPLICANT: Onrust, Rene

; APPLICANT: Kumble, Anand

; APPLICANT: Murison, Greg

; TITLE OF INVENTION: Compositions Isolated From Stromal Cells

; TITLE OF INVENTION: and Methods For Their Use

; FILE REFERENCE: 11000.1037c3

; CURRENT APPLICATION NUMBER: US/09/823,038A

; CURRENT FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 36

; LENGTH: 574

; TYPE: PRT

; ORGANISM: Mouse

; US-09-823-038A-36

Query Match 72.8%; Score 2197; DB 4; Length 574;

Best Local Similarity 70.7%; Pred. No. 6.3e-193;

Matches 403; Conservative 69; Mismatches 82; Indels 16; Gaps 2;

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QY 1 MECLYVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MESLGVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTS DSPALVGSNITFAVNLIPRCKOKEDANGNIYVEKNC 120
DB 61 VWRGEGRWKDSWEGGRVQAVLTS DSPALVGSNITFAVNLIPRCKOKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVNTWNTAMSEDSGNGTQSHHNVFPDGPFPHPGRRWFIYVFHTL 180
DB 121 RNDGLTSLDHVYNTWNTAGADGWEDGTSQHLRFPDRPRPFRPHGKWKSVYVFHTL 180
QY 181 GOYFQKLGRCVSRYVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPV 240
DB 181 GOYFQKLGRCVSRYVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPV 240
QY 241 TMFQKDRNSDDETFLLKDLPIMFQVLIHDPVLSHFLNYSTINVKWFGDNTGLFVSTNHTN 300
DB 241 TMSQKDRNSDDETFLLKDLPIMFQVLIHDPVLSHFLNYSTINVKWFGDNTGLFVSTNHTN 300
QY 301 HTYVLNGTFSNLTVAARPGCP-----PPPPPPR-----SKTPSLGPAGD 344
DB 301 HTYVLNGTFSNLTVAARPGCP-----PPPPPPR-----SKTPSLGPAGD 344
QY 345 NPLESRIPDENCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIQVVTVC 404
DB 345 NPLESRIPDENCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIQVVTVC 404
QY 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMTPOFANSLMDFTVTC 420
DB 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMTPOFANSLMDFTVTC 420
QY 405 QGSIPTEVCTIISDPTCEITQNTGSPVDVDMCLLTIVRRTPNGSGTCVNLTLGDDTSL 464
DB 405 QGSIPTEVCTIISDPTCEITQNTGSPVDVDMCLLTIVRRTPNGSGTCVNLTLGDDTSL 464
QY 421 KGATMEACTIISDPTCQIAQRVCSVPAVDGLCLLSVRRFNGSGTCVNLTLGDDTSL 480
DB 421 KGATMEACTIISDPTCQIAQRVCSVPAVDGLCLLSVRRFNGSGTCVNLTLGDDTSL 480
QY 465 ALTSTLISVPRDPAASPERMANSALISVGCIAIFVTIVSLIYKHKBYNFIENSPGNV 524
DB 465 ALTSTLISVPRDPAASPERMANSALISVGCIAIFVTIVSLIYKHKBYNFIENSPGNV 524
QY 481 ALTSTLISIPKDPSPRAVNGVLISIGCLAVLTMTVITLLYKHKYKPIGNCPRTV 540
DB 481 ALTSTLISIPKDPSPRAVNGVLISIGCLAVLTMTVITLLYKHKYKPIGNCPRTV 540
QY 525 RSKGLSVFLNRAKAVFFPGNOEKDPLKNO 554
DB 525 RSKGLSVFLNRAKAVFFPGNOEKDPLKNO 554
QY 541 KGKGLSVLLSHAKAPFFRGDQEKDPLQDK 570
DB 541 KGKGLSVLLSHAKAPFFRGDQEKDPLQDK 570
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RESULT 12

US-09-197-970B-5

; Sequence 5, Application US/09197970B

; Patent No. 6664385

; GENERAL INFORMATION:

; APPLICANT: Michele Sanicola-Nadel

Joseph V. Bonventre
Catherine A. Hession
Takaharu Ichimura
Henry Wei
Richard L. Cate
TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,970B
FILING DATE: 23-No. 6664385-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie M.
REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-197-970B-5

Query Match 72.0%; Score 2179; DB 4; Length 572;

Best Local Similarity 69.7%; Pred. No. 2.8e-191;

Matches 396; Conservative 74; Mismatches 84; Indels 14; Gaps 1;

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QY 1 MECLYVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MESLGVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTS DSPALVGSNITFAVNLIPRCKOKEDANGNIYVEKNC 120
DB 61 VWRGEGRWKDSWEGGRVQAVLTS DSPALVGSNITFAVNLIPRCKOKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVNTWNTAMSEDSGNGTQSHHNVFPDGPFPHPGRRWFIYVFHTL 180
DB 121 RNDGLTSLDHVYNTWNTAGADGWEDGTSQHLRFPDRPRPFRPHGKWKSVYVFHTL 180
QY 181 GOYFQKLGRCVSRYVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPV 240
DB 181 GOYFQKLGRCVSRYVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPV 240
QY 241 TMFQKDRNSDDETFLLKDLPIMFQVLIHDPVLSHFLNYSTINVKWFGDNTGLFVSTNHTN 300
DB 241 TMSQKDRNSDDETFLLKDLPIMFQVLIHDPVLSHFLNYSTINVKWFGDNTGLFVSTNHTN 300
QY 301 HTYVLNGTFSNLTVAARPGCP-----PPPPPPR-----SKTPSLGPAGDNP 346
DB 301 HTYVLNGTFSNLTVAARPGCP-----PPPPPPR-----SKTPSLGPAGDNP 346
QY 347 LELSRIPDENCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIQVVTVC 406
DB 347 LELSRIPDENCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIQVVTVC 406
QY 361 MELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMTPOFANSLMDFTVTC 420
DB 361 MELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMTPOFANSLMDFTVTC 420
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74	QY	KGGRVAVLTSDSPALVGSNITFAVNLLIPRCQEKEDANGNIVYEKNCRNEAGLSADPYVY	133
52	Db	KGGRV--AVTSDS--AVGSNT--AVN-----RC--KQANGVY--KNCRN-AG-SAD-YY	94
134	QY	NWTAWSBDSGCEGTGQSHNVFPDGKPFPHPGWRWNFIYVFHTLGOYFOKLGRCSVR	193
95	Db	NWTAWS--DSDG-NGTG-SHENV-DGK---HHGWRWNVYHTGK-----GRCSVR	137
194	QY	VSVNTANVTLGPOLMETVTVRRHGRBAYPIAQKDVVVVTDQIPVTFMFOKNDRNSSDE	253
138	Db	VSVNTANYT-----GMVTVYRRGRAYV--AVKDVVVVTD-----VVTM--KNDRNSSD	183
254	QY	TFLKDLPIMFVLJHDSPLFNTSTINYKWSFGDNTGLFVSTNHTVNNHTVYLVNGTFLSNL	313
184	Db	K-----DMDVHD-SH-NYST-NYKWS-GDNTG--VSTNHTVNNHTV-NGTSN--	223
314	QY	TKVAAAQPCPPPPPPRPSKPTPSLCPAGDNPLELSRIPDENCOINRYGCHFQATITVE	373
224	Db	TKVAAA--GC-----RSKTSAGDN---SR---DMC--NRVGH---ATTWG	256
374	QY	GILEWIIQMTDVLMPVPWPESSLLIDFVVTCQGSIPTEVCTIIISDPTCEITQNTVCSVD	433
257	Db	-----VNMTDMV-----WSSD-----VVTG-GS-----TVCTSDTC--TWTVGS-V	290
434	QY	VDENCLLTVRTPFNGSGTYCVNLTLGDDTSLATSLTISVDPDRDPASPLRMANSALISVG	493
291	Db	VD-MC--TVRRT-NGSGTYCVN--TGGDDTSATSTSV-----DRDAS--RWANSA--SVG	334
494	QY	CLAIPTVTVISLLVYKCKHEYNPIENSQGNVVRSKGLSVFLNRAKAVFPFGNQEBKPLKN	553
335	Db	C-----AVTVSVYKCHK-----YNNSGNVVRSGK---SVNRAKAV--GNKDKN----	372
554	QY	QEFKGVS	560
373	Db	---KGVS	376

q

```

314 TVKAAAFGCPGPPPPPPRPSKPTPSLGPAGDNPFLSLRIPDENQCINRVGHFQFQATITVE 373
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TVKAAA--GC-----RSKTSAGDN---SR---DNC--NRYGH-----ATTVG 256
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 GILEVNIQMTDVLMPVPPESSLIDFVVTCCQGSIPTEVCTIISDPTCEITQNTVCSPVD 433
: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
257 -----VNMSTDVWV-----WSSD-----VWTC--GS-----TVCTSDTC--TNTVCS--VD 290
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
434 VDEMLLTIVRRRTFNGSGTCYCNLTGLGDTSLALTSTLISVPDRDPASPLRMANSALISVG 493
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
291 VD-MC--TVRRT-NGSGTCYCN--TGGDTSATSTSV-----DRDAS--RMANSA--SVG 334
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
494 CLAFVTVVISLLVYKHKEYNPIENSPGNVVRKGLSVFLNRAKAVFFPGNOEKDPLLN 553
:: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
335 C-----AVTVSVYKXHK-----YNNSGNVVRSKG---SVNRAKAV---GNKDKN----- 372
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
554 QEFKGVGS 560
|||||
373 ---XGVGS 376
|||||

RESULT 14
US-09-985-799-102
; Sequence 102. Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/985,799
; FILING DATE: 06-No. RE38392-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Renenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TRUFAX: 202-639-7890

```

FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890

```

;
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 376 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-985-799-102

Query Match      32.0%; Score 969; DB 1; Length 376;
Best Local Similarity 54.5%; Pred. No. 1.8e-80;
Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;

QY 14 AARLPDAAKRFHDLGNRPSAYMRHNLQMGSSDENWNEKLYPVKRGDMRWKNSW 73
Db 6 AAR---DAAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWNKY---VKRGDMRWKNSW 51
QY 74 KGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYVEKNCNEAGLSADPYVY 133
Db 52 KGRV--AVTSDS--AVGNT--AVN---RC--KDANGNVY--KNCRN-AG-SAD-VYV 94
QY 134 NWTAWSEDGNGTGQSHHNVFPDGPFPHPHGRWRWFIYVPHTLGQYFQKLGRCVSR 193
Db 95 NWTAW--DSDG-NGTG-SHHNV--DGK---HHGWRWRWYVHTGYK-----GRCSVR 137
QY 194 VSVNTANVTLGQPMLEVTYRRHGRAYVPIAOKDVVYVTDQIPFVVTMFQKNDNSDE 253
Db 138 VSVNTANVT-----GMVTYRRHGRAYV--AVKDVVYVTD---VVTM--KNDNSD 183
QY 254 TFLKDLPIMDVLHDPHFNLNYSTINYKWSFGDNTGLFVSTNHTVNTHTYVLTGFSNL 313
Db 184 K-----DMDVHD-SH--NYST-NYKWS-GDNTG--VSTNHTVNTHTYV-NGTSN--- 223
QY 314 TVKAAAPGCPPPPPPPRPSKPTSLGPDAGNPLESRIPDENQINRYGHFOATITVE 373
Db 224 TVKAAA--GC-----RSKTSAGDN-----SR---DNC--NRYGH-----ATTVG 256
QY 374 GILEVNIQMTDVLMPVPWPESSLDIFVVTGCGSIPTVCTIISDPTCEITONTVCSPVD 433
Db 257 -----VNMTDMV-----WSSD-----VVC-GS-----TVCTSDTC---TNTVCS-VD 290
QY 434 VDEMCLLTVRTFNGSGTYCVNLTLDGDTSLALTSTLISVPRDRDPASPLRMANSALISVG 493
Db 291 VD-MC--TVRRT-NGSGTYCVN--TGDDTSATSTSV-----DRDAS---RMANSA--SVG 334
QY 494 CLAIPTVTISLLVKKHKEYNPIENSPGNVRSKGLSVFLNRAKAVFPFGNQEKDPLLN 553
Db 335 C-----AVTSVYKKHK-----YNSGNVRSKGLSVFLNRAKAV---GNKDKN----- 372
QY 554 QEFKGSV 560
Db 373 ---KGVS 376

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RESULT 15

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US-09-977-371-100
; Sequence 100, Application US/09977371
; Patent No. RE38490
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC

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; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,371
; FILING DATE: 16-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 376 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-977-371-100

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Query Match      32.0%; Score 969; DB 1; Length 376;
Best Local Similarity 54.5%; Pred. No. 1.8e-80;
Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;

QY 14 AARLPDAAKRFHDLGNRPSAYMRHNLQMGSSDENWNEKLYPVKRGDMRWKNSW 73
Db 6 AAR---DAAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWNKY---VKRGDMRWKNSW 51
QY 74 KGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYVEKNCNEAGLSADPYVY 133
Db 52 KGRV--AVTSDS--AVGNT--AVN---RC--KDANGNVY--KNCRN-AG-SAD-VYV 94
QY 134 NWTAWSEDGNGTGQSHHNVFPDGPFPHPHGRWRWFIYVPHTLGQYFQKLGRCVSR 193
Db 95 NWTAW--DSDG-NGTG-SHHNV--DGK---HHGWRWRWYVHTGYK-----GRCSVR 137
QY 194 VSVNTANVTLGQPMLEVTYRRHGRAYVPIAOKDVVYVTDQIPFVVTMFQKNDNSDE 253
Db 138 VSVNTANVT-----GMVTYRRHGRAYV--AVKDVVYVTD---VVTM--KNDNSD 183
QY 254 TFLKDLPIMDVLHDPHFNLNYSTINYKWSFGDNTGLFVSTNHTVNTHTYVLTGFSNL 313
Db 184 K-----DMDVHD-SH--NYST-NYKWS-GDNTG--VSTNHTVNTHTYV-NGTSN--- 223
QY 314 TVKAAAPGCPPPPPPPRPSKPTSLGPDAGNPLESRIPDENQINRYGHFOATITVE 373
Db 224 TVKAAA--GC-----RSKTSAGDN-----SR---DNC--NRYGH-----ATTVG 256
QY 374 GILEVNIQMTDVLMPVPWPESSLDIFVVTGCGSIPTVCTIISDPTCEITONTVCSPVD 433
Db 257 -----VNMTDMV-----WSSD-----VVC-GS-----TVCTSDTC---TNTVCS-VD 290
QY 434 VDEMCLLTVRTFNGSGTYCVNLTLDGDTSLALTSTLISVPRDRDPASPLRMANSALISVG 493
Db 291 VD-MC--TVRRT-NGSGTYCVN--TGDDTSATSTSV-----DRDAS---RMANSA--SVG 334

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Mon Nov 22 09:25:53 2004

Qy	494	CLAIPTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVFFPGNOEKDPLLN	553
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Qy	554	QEFKGV	560
Db	373	---RGVS	376

Search completed: November 19, 2004, 15:00:38
Job time : 41 secs